

811	10.6	39.3	24	AB01404	Human CYP11B gene
812	10.6	39.3	24	AB01405	Human CYP11B gene
813	10.6	39.3	24	AB01406	Human CYP11B gene
814	10.6	39.3	24	AB01407	Human CYP11B gene
815	10.6	39.3	24	AB01408	Human CYP11B gene
816	10.6	39.3	24	AB01409	Human CYP11B gene
817	10.6	39.3	24	AB01410	Human CYP11B gene
818	10.6	39.3	24	AB01411	Human CYP11B gene
819	10.6	39.3	24	AB01412	Human CYP11B gene
820	10.6	39.3	24	AB01413	Human CYP11B gene
821	10.6	39.3	24	AB01414	Human CYP11B gene
822	10.6	39.3	24	AB01415	Human CYP11B gene
823	10.6	39.3	24	AB01416	Human CYP11B gene
824	10.6	39.3	24	AB01417	Human CYP11B gene
825	10.6	39.3	24	AB01418	Human CYP11B gene
826	10.6	39.3	24	AB01419	Human CYP11B gene
827	10.6	39.3	24	AB01420	Human CYP11B gene
828	10.6	39.3	24	AB01421	Human CYP11B gene
829	10.6	39.3	24	AB01422	Human CYP11B gene
830	10.6	39.3	24	AB01423	Human CYP11B gene
831	10.6	39.3	24	AB01424	Human CYP11B gene
832	10.6	39.3	24	AB01425	Human CYP11B gene
833	10.6	39.3	24	AB01426	Human CYP11B gene
834	10.6	39.3	24	AB01427	Human CYP11B gene
835	10.6	39.3	24	AB01428	Human CYP11B gene
836	10.6	39.3	24	AB01429	Human CYP11B gene
837	10.6	39.3	24	AB01430	Human CYP11B gene
838	10.6	39.3	24	AB01431	Human CYP11B gene
839	10.6	39.3	24	AB01432	Human CYP11B gene
840	10.6	39.3	24	AB01433	Human CYP11B gene
841	10.6	39.3	24	AB01434	Human CYP11B gene
842	10.6	39.3	24	AB01435	Human CYP11B gene
843	10.6	39.3	24	AB01436	Human CYP11B gene
844	10.6	39.3	24	AB01437	Human CYP11B gene
845	10.6	39.3	24	AB01438	Human CYP11B gene
846	10.6	39.3	24	AB01439	Human CYP11B gene
847	10.6	39.3	24	AB01440	Human CYP11B gene
848	10.6	39.3	24	AB01441	Human CYP11B gene
849	10.6	39.3	24	AB01442	Human CYP11B gene
850	10.6	39.3	24	AB01443	Human CYP11B gene
851	10.6	39.3	24	AB01444	Human CYP11B gene
852	10.6	39.3	24	AB01445	Human CYP11B gene
853	10.6	39.3	24	AB01446	Human CYP11B gene
854	10.6	39.3	24	AB01447	Human CYP11B gene
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856	10.6	39.3	24	AB01449	Human CYP11B gene
857	10.6	39.3	24	AB01450	Human CYP11B gene
858	10.6	39.3	24	AB01451	Human CYP11B gene
859	10.6	39.3	24	AB01452	Human CYP11B gene
860	10.6	39.3	24	AB01453	Human CYP11B gene
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862	10.6	39.3	24	AB01455	Human CYP11B gene
863	10.6	39.3	24	AB01456	Human CYP11B gene
864	10.6	39.3	24	AB01457	Human CYP11B gene
865	10.6	39.3	24	AB01458	Human CYP11B gene
866	10.6	39.3	24	AB01459	Human CYP11B gene
867	10.6	39.3	24	AB01460	Human CYP11B gene
868	10.6	39.3	24	AB01461	Human CYP11B gene
869	10.6	39.3	24	AB01462	Human CYP11B gene
870	10.6	39.3	24	AB01463	Human CYP11B gene
871	10.6	39.3	24	AB01464	Human CYP11B gene
872	10.6	39.3	24	AB01465	Human CYP11B gene
873	10.6	39.3	24	AB01466	Human CYP11B gene
874	10.6	39.3	24	AB01467	Human CYP11B gene
875	10.6	39.3	24	AB01468	Human CYP11B gene
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877	10.6	39.3	24	AB01470	Human CYP11B gene
878	10.6	39.3	24	AB01471	Human CYP11B gene
879	10.6	39.3	24	AB01472	Human CYP11B gene
880	10.6	39.3	24	AB01473	Human CYP11B gene
881	10.6	39.3	24	AB01474	Human CYP11B gene
882	10.6	39.3	24	AB01475	Human CYP11B gene
883	10.6	39.3	24	AB01476	Human CYP11B gene
884	10.6	39.3	24	AB01477	Human CYP11B gene
885	10.6	39.3	24	AB01478	Human CYP11B gene



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REFERENCE
1 (base 1 to 25)
AUTHORS
Johansen, E.M. Jr., Milbrandt, J.D., Kolchauer, P.T. and Lange, E.A.
TITLE
Phosphatidyl and related growth factors
JOURNAL
FASEB J. 17: 2213-2218, 2003
SOURCE
1. 25
/organism="unknown"
BASE COUNT
4 a 4 c 7 g 10 t
ORIGIN
Query Match 47.4% Score 12.8; DB 6; Length 25;
Best Local Similarity 97.5%; Pred. No. 5.4e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 3 CTGACGATACCTAAC 18
1 |||||
21 CTGACGATACCTAAC 6

RESULT 39
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LOCUS
AX044281
DEFINITION
Sequence from Patent WO0006773.
ACCESSION
AX044281
VERSION
AX044281.1 GI:11343159
KEYWORDS
SYNTHETIC CONSTRUCT
SYNTHETIC CONSTRUCT
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 26)
Wardass, J.D., Heaney, S.P., Fernick, A., Whitcombe, D.M., Little, S.,
Gibson, N.J., Theaker, J. and Stanger, C.P.
Method of detection of synthetic constructs in fungal leading to
resistance against anti-fungal agents
Patent: WO 0006773-A 93 09-NOV-2000;
ZENEGA LIMITED (GB)
FEATURES
Location/Qualifiers
1..26
/organism="synthetic construct"
/db_xref="taxon:12630"
/note="Primer"
BASE COUNT
9 a 5 c 4 g 8 t
ORIGIN
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Best Local Similarity 97.5%; Pred. No. 5.4e+05;
Matches 11; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 11 TACCTACGACCAAT 26
1 |||||
1 TACCTACGACCAAT 16

RESULT 40
E04445 28 bp DNA linear PAT 29 SEP-1997
LOCUS
E04445/c
DEFINITION
DNA encoding primer for detection of mutation at ornithine
transcarbamylase(OTC) gene.
ACCESSION
E04445
VERSION
E04445.1 GI:2172646
KEYWORDS
OT 199306800 A/5
SOURCE
synthetic construct.
SYNTHETIC CONSTRUCT
ORGANISM
artificial sequences.
REFERENCE
1 (bases 1 to 28)
Matsuda, I., Shimada, K. and Matsura, T.
OLIGONUCLEOTIDE AND DETECTION OF LAMININE 199306800A/5b MUTATED
GENE WITH THE SAME
Patent: JP 199306800-A 5 23-MAR-1993;
MATSUDA ICHIRO, SHIMADA KAZUMORI, MATSURA JOSHINOBU
OR Artificial gene
OR Artificial sequence; Genes.

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FN JP 199306800-A/5
FE 23 MAR 1993
FD 24 MAY 1993 OF 1993149718
FI MATSUDA ICHIRO, SHIMADA KAZUMORI, MATSURA JOSHINOBU
GI 2172646/Arise/OTC/Primer/OTC 199306800A/5b
ORIGIN
CC strandedness: Single;
CC topology: linear;
CC hypothetical: No;
CC anti-sense: No;
FEATURES
Location/Qualifiers
1..28
/note="synthetic construct"
/note="Primer"
BASE COUNT
6 a 4 c 6 g 12 t
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Best Local Similarity 70.8%; Pred. No. 5.4e+05;
Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 4 TGGCATACCTAACGACCAATA 27
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28 TGGCATACCTAACGACCAATA 5

Search completed: July 21, 2003, 14:35:09
Job time: 289.347 secs

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LOCUS 117731 20 bp DNA linear FAT 02-APR-1996
 DEFINITION Sequencer 6 from patient US 5693467
 ACCESSION 117731
 VERSION 117731.1 GI:1250619
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Masamichi, D. and Otsu, P. S.
 TITLE Characterized expression of non bacterial genes in bacterial cells
 JOURNAL Patent: US 5470127 A 5 28 NOV-1995;
 FEATURES
 SOURCE 1..20
 BASE COUNT 3 a 4 c 6 g 7 t
 ORIGIN
 Query Match 47.4% Score 12.8; DP 6; Length 20;
 Best Local Similarity 87.5% Pred No. 5,6e-05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CY 3 CTGACCAATACCTAAC 18
 DB 17 CTGACCAATACCTAGC 2
 RESULT 15
 LOCUS A98952/c 21 bp DNA linear FAT 26 JAN 2000
 DEFINITION 21 bases 1 to 21
 ACCESSION A98952
 VERSION A98952.1 GI:6781912
 KEYWORDS
 SOURCE unidentified;
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Albrecht, C. and Duster, J.
 TITLE METHOD FOR ENZYMATICALLY RECOGNIZING GUANOSINE
 DIPHOSPHATE 5-PHOSPHOTRANSFERS AND THE USE THEREOF FOR PRODUCING
 OLIGONUCLEOTIDES
 JOURNAL Patent: WO 9909180 A 13 25-FEB-1999;
 FEATURES
 SOURCE 1..21
 BASE COUNT 1 a 2 c 3 g 4 t
 ORIGIN
 Query Match 47.4% Score 12.8; DP 6; Length 21;
 Best Local Similarity 87.5% Pred No. 5,6e-05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CY 3 CTGACCAATACCTAAC 18
 DB 16 CTGACCAATACCTAGC 1
 RESULT 16
 LOCUS 176915 21 bp DNA linear FAT 03-APR-1998
 DEFINITION Sequencer 23 from patient US 5693467.
 ACCESSION 176915
 VERSION 176915.1 GI:3013069
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Roblin, P. O. III, H.W., Trogoff, S. and Lewis,
 TITLE Mycoplasma fermentans strain reduction testing system using a set of

LOCUS 117731 20 bp DNA linear FAT 02-APR-1996
 DEFINITION Sequencer 6 from patient US 5470127
 ACCESSION 117731
 VERSION 117731.1 GI:1250619
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 REFERENCE 1 (bases 1 to 20)
 AUTHORS Masamichi, D. and Otsu, P. S.
 TITLE Characterized expression of non bacterial genes in bacterial cells
 JOURNAL Patent: US 5470127 A 5 28 NOV-1995;
 FEATURES
 SOURCE 1..20
 BASE COUNT 3 a 4 c 6 g 7 t
 ORIGIN
 Query Match 47.4% Score 12.8; DP 6; Length 20;
 Best Local Similarity 87.5% Pred No. 5,6e-05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CY 3 CTGACCAATACCTAAC 18
 DB 17 CTGACCAATACCTAGC 2
 RESULT 15
 LOCUS A98952/c 21 bp DNA linear FAT 26 JAN 2000
 DEFINITION 21 bases 1 to 21
 ACCESSION A98952
 VERSION A98952.1 GI:6781912
 KEYWORDS
 SOURCE unidentified;
 ORGANISM unidentified
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Albrecht, C. and Duster, J.
 TITLE METHOD FOR ENZYMATICALLY RECOGNIZING GUANOSINE
 DIPHOSPHATE 5-PHOSPHOTRANSFERS AND THE USE THEREOF FOR PRODUCING
 OLIGONUCLEOTIDES
 JOURNAL Patent: WO 9909180 A 13 25-FEB-1999;
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 Query Match 47.4% Score 12.8; DP 6; Length 21;
 Best Local Similarity 87.5% Pred No. 5,6e-05;
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 CY 3 CTGACCAATACCTAAC 18
 DB 16 CTGACCAATACCTAGC 1
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 LOCUS 176915 21 bp DNA linear FAT 03-APR-1998
 DEFINITION Sequencer 23 from patient US 5693467.
 ACCESSION 176915
 VERSION 176915.1 GI:3013069
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Roblin, P. O. III, H.W., Trogoff, S. and Lewis,
 TITLE Mycoplasma fermentans strain reduction testing system using a set of

VERSION	APR9720.1	21-1704199
KEYWORDS	Unknown.	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 bases 1 to 10	
AUTHORS	Hartung, F., Barmann, C., W., Tegtmeyer, A., Giedl, J., and S. H. Hartung.	
TITLE	Delta-casein expressing constructs	
JOURNAL	Patent: US 6287845-A 16-11-97P-2001;	
FEATURES	Location/Qualifiers	
source	1..19	
BASE COUNT	3 a 4 c 6 g 6 t	
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Best Local Similarity	97.5%; Pred No. 6605;	
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DB	16 CTGAGCAATACCTAAC 1	
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DEFINITION	Sequence 6 from patent US 5861273.	NMA
ACCESSION	AR030433	
VERSION	AR030433.1	GI:5943647
KEYWORDS	Unproven	
SOURCE	Unknown.	
ORGANISM	Unclassified.	
REFERENCE	1 (bases 1 to 20)	
AUTHORS	Olsen, P.S. and Mascarenhas, D.	
TIME	Chromosomal expression of heterologous genes in bacterial cells	
JOURNAL	Patent: US 5861273.A 6-19-JAN-1999;	
FEATURES	Location/Qualifiers	
source	1..20	

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BASE COUNT      3 a      4 c      6 g      7 t
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Best Local Similarity 87.8% Fwd: N0.560+055
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27 CTGAGCAATACCTAGC 18
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17 CTGAGCAATACCTAGC 2

RESULT 32
AR030447/c      40 bp      LINA      Linear      DAT 29 SEP 1990
DDBS
DEFINITION
Accession      AR030447
VERSION
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 20)
Olson,P.S. and Mascarenhas,D.
Cloning and characterization of human T-cell leukemia virus
provirus sequences in a head-to-tail arrangement
Location/Qualifiers
1..20
/organism="unknown"

BASE COUNT      3 a      4 c      6 g      7 t
ORIGIN
Query Match      47.4% Score 12.87 DB 61 Length 201
Best Local Similarity 87.8% Fwd: N0.560+055
Matches 14, Conservative 0, Mismatched 4, Indels 0 Sps 0.00
27 CTGAGCAATACCTAGC 18
|||||
17 CTGAGCAATACCTAGC 2

RESULT 33
AR030449/c
DEFINITION
Accession      AR030449
VERSION
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 20)
Olson,P.S. and Mascarenhas,D.
Chemical expression of heterologous genes in bacterial cells
Patent US 5618733 A 01/19/90-1999;
Location/Qualifiers
1..20
/organism="unknown"

BASE COUNT      3 a      4 c      6 g      7 t
ORIGIN
Query Match      47.4% Score 12.87 DB 61 Length 201
Best Local Similarity 87.8% Fwd: N0.560+055
Matches 14, Conservative 0, Mismatched 4, Indels 0 Sps 0.00
27 CTGAGCAATACCTAGC 18
|||||
17 CTGAGCAATACCTAGC 2

RESULT 34
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 /db_xref="taxon:32436"
 /note="Polybasic Nucleic Acid"
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 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

cy 1 TTTTCAATCAATCAATCAAT 30
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 4 TCTGACCACTACCTACCACTAC 25

RESULT 25
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 LOCUS
 DEFINITION Sequence 9 from patent US 6180111
 ACCESSION ARI91267
 VERSION ARI91267.1 GI:14112840
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 Unclassified.
 REFERENCE 1 (bases 1 to 35)
 AUTHORS Stein,D.C. and Stover,C.K.
 TITLE Vaccine delivery system
 JOURNAL Patent: US 6180111-A 9 30 JAN-2001;
 FEATURES
 source location/Qualifiers
 1..35
 /organism="Unknown"
 BASE COUNT 16 a 3 c 6 g 10 t
 ORIGIN

Query Match 48.9% Score 13.2; DB 6; Length 31;
 Best Local Similarity 83.8% Pred. No. 3.5e+05;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

cy 9 AATCACTAATCAATCAAT 26
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 12 AATCACTAATCAATCAAT 25

RESULT 26
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 LOCUS
 DEFINITION Sequence 919 from Patent WO0151627.
 ACCESSION AXI97112
 VERSION AXI97112.1 GI:15387318
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 Unclassified.
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hupp,P.M., Wang,M.L., Parsons,D.P. and Fallahe,L.L.
 TITLE Human anti-metastases and other antibodies associated with myxian
 cyst nematode resistance
 JOURNAL Patent: WO 0151627-A 819 19 JUL-2001;
 FEATURES
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 1..25
 /organism="Glycine max"
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 318013 region A3_269358 15 Forward_Primer_Seq"
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cy 3 CTGACCACTACCTACCACTAC 23
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 25 CTGACCACTACCTACCACTAC 25

RESULT 27
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 ACCESSION ARI91268
 VERSION ARI91268.1 GI:20237233
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 Unclassified.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Pavesi,P., Meszky,M., Strohreich,P. and Reebhorst,
 TITLE Method and reagent for the treatment of diseases or conditions
 related to levels of vascular endothelial growth factor receptor
 JOURNAL Patent: US 6346398-A 676 17 FEB 2002;
 FEATURES
 source location/Qualifiers
 1..27
 /organism="Unknown"
 BASE COUNT 10 a 5 c 5 g 4 t
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Query Match 48.1% Score 13; DB 6; Length 27;
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 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

cy 6 AGCAATACCTACCACTACCA 27
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 1 AATCACTAATCAATCAATCA 22

RESULT 28
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 LOCUS
 DEFINITION Sequence 131 from patent US 6180341.
 ACCESSION ARI26504
 VERSION ARI26504.1 GI:14113097
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown
 Unclassified.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Johnson,P.L., George,J.G. and Burke,E.A.
 TITLE In vitro scanning saturation mutagenesis of proteins
 JOURNAL Patent: US 6180341-A 131 30 JAN-2001;
 FEATURES
 source location/Qualifiers
 1..19
 /organism="Unknown"
 BASE COUNT 3 a 4 c 6 g 6 t
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Query Match 47.4% Score 12.9; DB 6; Length 19;
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cy 3 CTGACCACTACCTAC 18
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 LOCUS
 DEFINITION Sequence 16 from patent US 6287866.
 ACCESSION ARI68720

Query Match 48.9% Score 13.2; DB 6; Length 27;
Best Local Similarity 69.2% Freq. No. 3.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0

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DB 26 CCTGAGCAATACCTAGCAACAAATA 1

RESULT 20
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LOCUS AR071820 48 bp. LNA
DEFINITION Sequence 11 from patent US 5912148.
ACCESSION AR071820
VERSION AR071820.1 GI:14692460
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Eggerding,F.
TITLE Cloned amplification and ligation method
JOURNAL Patent: US 5912148-A 11-10-OCT-1999;
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Source 1..28
/organism="unknown"

BASE COUNT 13 a 7 c 5 g 3 t
ORIGIN

Query Match 48.9% Score 13.2; DB 6; Length 29;
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Matches 18; Conservative 0; Mismatches 8; Indels 0

QY 2 CCTGAGCAATACCTAGCAACAAATA 27
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DB 2 CCTGAGCAATACCTAGCAACAAATA 27

RESULT 21
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LOCUS AR066438 48 bp. LNA
DEFINITION Sequence 11 from patent US 5912148.
ACCESSION AR066438
VERSION AR066438.1 GI:14691904
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 28)
AUTHORS Nixon,S.A., Catala,A.M., Kay,B.H. and Matthews,P.M.
TITLE Use of presentin-1 for diagnosis of alzheimers disease
JOURNAL Patent: US 59581-A 7-16-OCT-1999;
FEATURES
Source 1..28
/organism="unknown"

BASE COUNT 7 a 9 c 7 g 5 t
ORIGIN

Query Match 48.9% Score 13.2; DB 6; Length 29;
Best Local Similarity 69.2% Freq. No. 3.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0

QY 2 CCTGAGCAATACCTAGCAACAAATA 19
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DB 11 CCTGAGCAATACCTAGCAAC 28

RESULT 22
AR112560
LOCUS AR112560 49 bp. LNA
DEFINITION Sequence 11 from patent US 5912148.
ACCESSION AR112560

VERSION AR112560.1 GI:14692460
KEYWORDS
SOURCE Unknown.
DEFINITION
REFERENCE 1 (bases 1 to 28)
AUTHORS Eggerding,F.
TITLE Cloned amplification and ligation method
JOURNAL Patent: US 5912148-A 11-10-OCT-2000;
FEATURES
Source 1..28
/organism="unknown"

BASE COUNT 13 a 7 c 5 g 3 t
ORIGIN

Query Match 48.9% Score 13.2; DB 6; Length 27;
Best Local Similarity 69.2% Freq. No. 3.5e+05;
Matches 18; Conservative 0; Mismatches 8; Indels 0

QY 2 CCTGAGCAATACCTAGCAACAAATA 27
|||||
DB 2 CCTGAGCAATACCTAGCAACAAATA 27

RESULT 23
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LOCUS AX278206 30 bp. LNA
DEFINITION Sequence 17 from Patent WO0177553.
ACCESSION AX278206
VERSION AX278206.1 GI:16605257
KEYWORDS
SOURCE Synthetic construct.
ORGANISM Synthetic construct.
REFERENCE 1
AUTHORS Heifetz,P.B., Goff,S.A., Tuttle,A.B. and Gross,West,M.E.
TITLE Effected by either allele in placenta
JOURNAL Patent: WO 0177553-A 17-10-OCT-2001;
FEATURES
Source 1..30
/organism="Synthetic construct"
/note="oligonucleotide"

BASE COUNT 11 a 6 c 7 g 5 t
ORIGIN

Query Match 48.9% Score 13.2; DB 6; Length 37;
Best Local Similarity 69.2% Freq. No. 3.5e+05;
Matches 13; Conservative 0; Mismatches 3; Indels 0

QY 1 TCTTAGCAATACCTAGC 18
|||||
DB 9 TCTTAGCAATACCTAGC 26

RESULT 24
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LOCUS AX425555 21 bp. LNA
DEFINITION Sequence 11 from WO 98/05124.
ACCESSION AX425555
VERSION AX425555.1 GI:1529937
KEYWORDS
SOURCE Synthetic construct.
ORGANISM Synthetic construct.
REFERENCE 1
AUTHORS Jarvis,T., von Garlowitz,I., Meswigen,J.A., Melantheim,F.G. and Randi,A.M.
TITLE Method and reagent for the inhibition of eeg
JOURNAL Patent: WO 9805124 A 1991-02-01;
FEATURES
Source 1..21
/organism="Synthetic construct"
/note="oligonucleotide"

ORGANISM Unknown.
Unclassified.

REFERENCE 1 (bases 1 to 22)
AUTHORS Chachchach, P.T., Praparak, W., Chachchach, and Chachchach, T.
TITLE Camp Engraved Ribosomes
JOURNAL Nucleic Acids Res 2002;30:1111-1116
FEATURES
SOURCE 1
BASE COUNT 2 a 2 g 2 j 11
ORIGIN

Query Match 50.4%; Score 13.6; DB 6; Length 22
Best Local Similarity 70.9%; Pred. No. 3; Len 22
Matches 16, Conservative 0, Mismatches 6, Indels 0, Gaps 0

QY 2 CCTAGCAATACCTACGAA 21
DB 22 CCTAGCAATACCTACGAA 3

RESULT 13
AX119563
LOCUS AX119563
DEFINITION Sequence 220 from Patent WO0129251.
ACCESSION AX119563
VERSION AX119563.1 GI:14036482
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; 1 (bases 1 to 15)
AUTHORS Messiaen, L. and Callens, T.
TITLE Improved mutation analysis of the 15 gene
JOURNAL Famc. Wc 2002;11 A 262-267-2002
UNIVERSITY GENE (FR)
FEATURES
SOURCE Location/Qualifiers
1..15
BASE COUNT 2 a 2 g 3 g 9 t
ORIGIN

Query Match 49.6%; Score 13.4; DB 6; Length 15
Best Local Similarity 93.3%; Pred. No. 3; Len 15
Matches 14, Conservative 0, Mismatches 1, Indels 0, Gaps 0

QY 13 CCTAGCAATACCTACGAA 27
DB 15 CCTAGCAATACCTACGAA 1

RESULT 14
E33644
LOCUS E33644
DEFINITION Protein binding to Pz, Pz encoding the protein and antibody
ACCESSION E33644
VERSION E33644.1 GI:18624143
KEYWORDS JP 2000093179-A/4.
SOURCE synthetic construct.
ORGANISM artificial sequences.
1 (bases 1 to 27)
REFERENCE 1
AUTHORS Kishimoto, T., Yamane, K., Nakamura, T., Taira, T. and Taira, T.
TITLE Protein binding to Pz, Pz encoding the protein and antibody
JOURNAL Famc. Wc 2000;93179-A 4 04-Apr-2000
SCIENTIFIC ELECTRIC IND LTD
OS Artificial Sequence
PN JP 2000093179-A/4
PD 04 APR-2000

PF 24-SEP-1998 JP 199809192
PR
E1 TOCHIMURA KISHIMOTO, TOSHIO KAWAMURA, TOSHIKI NAKAMURA, TOSHIO
E2 SHINICHIRO YAMANE,
E3 TORU YAKUMI
E4
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E100

FEATURES
SOURCE Location/Qualifiers
1..27
BASE COUNT 9 a 9 g 5 g 4 t
ORIGIN

Query Match 49.6%; Score 13.4; DB 6; Length 27
Best Local Similarity 70.9%; Pred. No. 3; Len 27
Matches 17, Conservative 0, Mismatches 6, Indels 0, Gaps 0

QY 5 CAGCAATACCTACGAA 27
DB 4 CAGCAATACCTACGAA 26

RESULT 15
AX378524
LOCUS AX378524
DEFINITION Sequence 270 from Patent WO020025.
ACCESSION AX378524
VERSION AX378524.1 GI:12574377
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo; 1 (bases 1 to 18)
AUTHORS Cohen, P., Blumenfeld, M., Chumakov, I., Akbarian, S. and Blumenfeld, P.
TITLE Obesity associated diallelic marker maps
JOURNAL Famc. Wc 2002;11 A 213-214-2002
GENSET (FR)
FEATURES
SOURCE Location/Qualifiers
1..18
BASE COUNT 7 a 7 g 1 g 3 t
ORIGIN

Query Match 48.9%; Score 13.2; DB 6; Length 18
Best Local Similarity 93.3%; Pred. No. 3; Len 18
Matches 15, Conservative 0, Mismatches 3, Indels 0, Gaps 0

QY 1 TCTTAGCAATACCTACG 18
DB 1 TCTTAGCAATACCTACG 18

RESULT 16
AR031466
LOCUS AR031466
DEFINITION Sequence 24 from Patent WO 980363.
ACCESSION AR031466
VERSION AR031466.1 GI:15945755
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 21)
UNCLASSIFIED.

RESULT 5			
AX081643	AX081643	33 bp	DNA
LOCUS			1 line
DEFINITION	Sequence 18 from E. coli W 1000000		
ACCESSION	AF061643		
VERSION	AX081643.1	GI:1317068	
KEYWORDS			
SOURCE	Synthetic construct.		
ORGANISM	Escherichia coli		
REFERENCE	Artificial sequences.		
	1. (bases 1 to 33)		

DEFINITION	Exposure 500' from Present W020333708
ACCESSION	AX468217
VERSION	AX468217.1 GI:22322257
KEYWORDS	
SOURCE	
ORGANISM	

REFERENCE	AUTHORS	TITLE	YEAR	ORGANIZATION	FEATURES
1	Poernery, T., Tang, B., Egeberg, C., Rusevsky, H., and Christensen, H.	Gene disruption methodologies for drug target discovery	2002	Novartis	Phlora Pharmaceuticals, Inc. (US) Location/Qualifiers

C 942	10	37.0	17	6	AR034147	AR034147 Sequence
C 943	10	37.0	17	6	AX008976	AX008976 Sequence
C 944	10	37.0	17	6	ED005941	ED005941 Cephalop
C 945	10	37.0	17	6	173159	173159 Sequence 21
C 946	10	37.0	18	6	AR049844	AR049844 Sequence
C 947	10	37.0	18	6	AR045532	AR045532 Sequence
C 948	10	37.0	18	6	AR140362	AR140362 Sequence
C 949	10	37.0	18	6	AR160417	AR160417 Sequence
C 950	10	37.0	18	6	AR160841	AR160841 Sequence
C 951	10	37.0	18	6	AR181657	AR181657 Sequence
C 952	10	37.0	18	6	ED004274	ED004274 Remedy of
C 953	10	37.0	18	6	ED008988	ED008988 Spis Poly
C 954	10	37.0	18	6	ED009201	ED009201 Novel 3p
C 955	10	37.0	18	6	AA9212	AA9212 Sequence 2
C 956	10	37.0	19	6	AR000157	AR000157 Sequence
C 957	10	37.0	19	6	AR049727	AR049727 Sequence
C 958	10	37.0	19	6	AR053054	AR053054 Sequence
C 959	10	37.0	19	6	AX130030	AX130030 Sequence
C 960	10	37.0	19	6	AX130540	AX130540 Sequence
C 961	10	37.0	19	6	AX133921	AX133921 Sequence
C 962	10	37.0	19	6	AX133257	AX133257 Sequence
C 963	10	37.0	19	6	AX132258	AX132258 Sequence
C 964	10	37.0	19	6	AX352994	AX352994 Sequence
C 965	10	37.0	19	6	AX362839	AX362839 Sequence
C 966	10	37.0	19	6	133664	133664 Sequence 7
C 967	10	37.0	19	6	165452	165452 Sequence 8
C 968	10	37.0	19	6	ED011212	ED011212 Sequence
C 969	10	37.0	19	6	AA4454	AA4454 Sequence 22
C 970	10	37.0	20	6	AA4654	AA4654 Sequence 30
C 971	10	37.0	20	6	AR032106	AR032106 Sequence
C 972	10	37.0	20	6	AR049093	AR049093 Sequence
C 973	10	37.0	20	6	AR032635	AR032635 Sequence
C 974	10	37.0	20	6	AR104403	AR104403 Sequence
C 975	10	37.0	20	6	AR106948	AR106948 Sequence
C 976	10	37.0	20	6	AR139457	AR139457 Sequence
C 977	10	37.0	20	6	AR156337	AR156337 Sequence
C 978	10	37.0	20	6	AR178816	AR178816 Sequence
C 979	10	37.0	20	6	AR207137	AR207137 Sequence
C 980	10	37.0	20	6	AX339154	AX339154 Sequence
C 981	10	37.0	20	6	AX138976	AX138976 Sequence
C 982	10	37.0	20	6	AX206728	AX206728 Sequence
C 983	10	37.0	20	6	AX294558	AX294558 Sequence
C 984	10	37.0	20	6	AX294137	AX294137 Sequence
C 985	10	37.0	20	6	AX400954	AX400954 Sequence
C 986	10	37.0	20	6	AX348171	AX348171 Sequence
C 987	10	37.0	20	6	AX339189	AX339189 Sequence
C 988	10	37.0	20	6	ED011212	ED011212 Sequence
C 989	10	37.0	20	6	ED011212	ED011212 Sequence
C 990	10	37.0	20	6	ED011212	ED011212 Sequence
C 991	10	37.0	21	6	AR041200	AR041200 Sequence
C 992	10	37.0	21	6	AR041200	AR041200 Sequence
C 993	10	37.0	21	6	AR041200	AR041200 Sequence
C 994	10	37.0	21	6	AR054267	AR054267 Sequence
C 995	10	37.0	21	6	AR054469	AR054469 Sequence
C 996	10	37.0	21	6	AR115503	AR115503 Sequence
C 997	10	37.0	21	6	AR154090	AR154090 Sequence
C 998	10	37.0	21	6	AR159952	AR159952 Sequence
C 999	10	37.0	21	6	AR164544	AR164544 Sequence
C1000	10	37.0	21	6	AR182857	AR182857 Sequence

ALIGNMENTS

RESULT 1
 LOCUS AX032926 27 bp DNA linear PAT 21-SEP-2003
 DEFINITION AX032926
 ACCESSION AX032926
 VERSION AX032926.1 GI:10674900
 KEYWORDS
 SOURCE
 ORGANISM Synthetic construct

REFERENCE
 1 (Pages 1 to 27)
 AUTHORS Beckert, D. and Green, C.R.
 TITLE Formulations comprising anti-insect proteins for pest control
 JOURNAL Patent WO 0044900A 4 (2000)
 REENTRY LAMBERT (2001) ; TRIV LAMBERT (2001) ; GREEN (2001) ; (N2)
 LOCATION/Qualifiers
 1..27
 /organism "Synthetic Construct"
 /db_xref="taxon:4240"
 /note="Polynucleotide"
 BASE COUNT 12 a 7 c 3 g 5 t
 ORIGIN

Query Match 100.0% Score 27.0 E-67 Length 27
 Best Local Similarity 100.0% E-67 Length 27
 Matches 27/ Conservative 0 Mismatches 0 Gaps 0

27
 1 TCGTAAAGTAACTTAAAGTAAATA 27
 |||
 1 TCGTAAAGTAACTTAAAGTAAATA 27

RESULT 2
 LOCUS AR120372/C 45 bp DNA linear PAT 16 MAY 2001
 DEFINITION AR120372
 ACCESSION AR120372
 VERSION AR120372.1 GI:14103948
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (Pages 1 to 35)
 AUTHORS Beckert, D., Green, C.R., Fannon, M.R., and Posen, C.A.
 TITLE Formulations comprising anti-insect proteins for pest control
 JOURNAL Patent WO 0044900A 4 (2000)
 REENTRY LAMBERT (2001) ; TRIV LAMBERT (2001) ; GREEN (2001) ; (N2)
 LOCATION/Qualifiers
 1..35
 /organism "Unknown"
 BASE COUNT 3 a 5 c 11 g 16 t
 ORIGIN

Query Match 56.8% Score 15.0 E-67 Length 35
 Best Local Similarity 79.1% E-67 Length 35
 Matches 18/ Conservative 0 Mismatches 5 Gaps 0

27
 1 GATTAATATATATATATATATATAT 27
 |||
 34 GATTAATATATATATATATATATAT 12

RESULT 3
 LOCUS ED01025 36 bp DNA linear PAT 29 SEP 1997
 DEFINITION ED01025
 ACCESSION ED01025
 VERSION ED01025.1 GI:1419284
 KEYWORDS
 UP 1986274684 A/1.
 SOURCE Synthetic construct.
 ORGANISM Synthetic construct.
 REFERENCE 1 (bases 1 to 35)
 AUTHORS Tsuchiya, M., Watanabe, Y., Yamaguchi, T., Yamaguchi, A., Watanabe, K., and Sano, T.
 TITLE METHOD OF HAVING A SEQUENCE OF A SYNTHETIC POLYMER
 JOURNAL Patent JP 1986274684 A 1 (1986)
 ACCESSION ED01025
 ORIGIN
 OS Artificial gene.
 OC Artificial sequence; Genes.
 IN CF 1986274684 A/1

[illegible]

with adapters complementary to the insect adapters and purified. The sheared, adaptered mouse DNA was annealed to adaptered vector DNA, and transformed into chemically-competent *E. coli* Xho-3d3 (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT	14 d	10 c	3 q	2 f
ORIGIN				

ORIGIN

Query Match	38.78	Score 11.6	DB 17	Length 29
Best Local Similarity	77.8	Pred. No. 1.3e+06		
Matches 14	Conservative 0	Mismatches 4	Indels 0	Gaps 0

5' ATGAGACACCCAAAGACACT 22

Idb 9 ACACACCAAGATACT 26

Search completed: July 21, 2003, 15:47:29
Job time : 799.76 secs

adaptor DNA was purified and size selected for a 3.2 kb 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pCR4.3 (Invitrogen) by substituting a 3.2 kb fragment of the vector with the complementary to the insert adapters and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT
ORIGIN
Query Match 100% Score 11.5 E-11 Length 19
Best local similarity 77.8% from 1 to 19
Matches 14, Conservation 0, Mismatches 4, Indels 0, Gaps 0

12 CCAGAGACCTACACCA 29
11 | | | | | | | | | |
19 CCAGACACCTACACCA 2
11 | | | | | | | | | |

RESULT 35
AZ51324/0
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
MUS MUSCULUS
Mus musculus
Eukaryota, Mammalia, Chiroptera, Eulipotyphla, Eulipotyphli, Muridae, Murinae, Murini, Mus
1 (bases 1 to 21)
Author: Ayala, R., Barker, M., Beaudry, J., Daulton, T., Hamby, J., Ismail, H., Longacre, S., Marmorek, M., Mendenhall, J., Peltz, M., Rose, M., Rose, P., Sikes, P., Tinsley, A., von Niederhausern, A., and Wright, D., Weiss, R.
Mice whole genome scaffolding with BAC and YAC from 1998
Plasmid inserts
Established library
Genotype: P. Weiss
University of Utah Genome Center
Salt Lake City, Utah 84112, USA
Tel: 801 581 5406
Fax: 801 581 7177
Email: dmu@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0353 Low 0 column 23
Seq primer: CAGACGAGACCTACACCA
Class: Plasmid ends
High quality sequence stop: 21

FEATURE
SOURCE
1..21
/organism="Mus musculus"
/strain="P. Weiss"
/db_xref="taxon:10090"
/clone="musmus000001"
/contig="100000000000"
/contig="100000000000"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, P. Weiss"
/notes="Vector: pCR4.3, Purified genomic DNA from M. musculus (GRI/AT) (male) was obtained from the Jackson Laboratory Mouse DNA Resource
The 1.7 kb fragment of the vector was substituted into the 3.2 kb fragment of the vector by repeated ligations through a 0.1 kb fragment of the vector. The sheared DNA was blunt ended and ligated with 74 DNA polymerase and 74 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The

BASE COUNT
ORIGIN
Query Match 100% Score 11.5 E-11 Length 19
Best local similarity 77.8% from 1 to 19
Matches 14, Conservation 0, Mismatches 4, Indels 0, Gaps 0

12 CCAGAGACCTACACCA 29
11 | | | | | | | | | |
19 CCAGACACCTACACCA 2
11 | | | | | | | | | |

RESULT 36
AZ51319/0
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
MUS MUSCULUS
Mus musculus
Eukaryota, Mammalia, Chiroptera, Eulipotyphla, Eulipotyphli, Muridae, Murinae, Murini, Mus
1 (bases 1 to 21)
Author: Ayala, R., Barker, M., Beaudry, J., Daulton, T., Hamby, J., Ismail, H., Longacre, S., Marmorek, M., Mendenhall, J., Peltz, M., Rose, M., Rose, P., Sikes, P., Tinsley, A., von Niederhausern, A., and Wright, D., Weiss, R.
Mice whole genome scaffolding with BAC and YAC from 1998
Plasmid inserts
Established library
Genotype: P. Weiss
University of Utah Genome Center
Salt Lake City, Utah 84112, USA
Tel: 801 581 5406
Fax: 801 581 7177
Email: dmu@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0442 Low 0 column 01
Seq primer: CAGACGAGACCTACACCA
Class: Plasmid ends
High quality sequence stop: 25

FEATURE
SOURCE
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/organism="Mus musculus"
/strain="P. Weiss"
/db_xref="taxon:10090"
/clone="musmus000001"
/contig="100000000000"
/contig="100000000000"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, T1-resistant, P. Weiss"
/notes="Vector: pCR4.3, Purified genomic DNA from M. musculus (GRI/AT) (male) was obtained from the Jackson Laboratory Mouse DNA Resource
The 1.7 kb fragment of the vector was substituted into the 3.2 kb fragment of the vector by repeated ligations through a 0.1 kb fragment of the vector. The sheared DNA was blunt ended and ligated with 74 DNA polymerase and 74 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The


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Insert length: 16000      Std Error: 6.00
Plate: 0013      Row: H      Column: 13
Seq primer: ATTGTAAGAAAGTACATGAT
Class: plasmid ends
High quality sequence strop: 34.
Total input: 20000000

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2 a 4 C 3 g 25 t

BASE COUNT	2 a	4 c	3 g	25 t
ORIGIN				

Query Match	40.78	57.14	60.71	67.17	Length 34.
Best local alignment	69.09	100.00	100.00	100.00	
Matches	17	Conservative	9	Indels	0
		Mismatches	9	Gaps	0

DY 2 GGTATATAGTACCAAGACACTAACA 2
| | | | |
Db 28 GTTAGAGTTAAAAAGAAATACTA 4

RESULT 24

A631678170

16-01

DEFINITION 1.

ACCESSION

VERSION:

KFVW-TV

SOURCE

ORGANIS

REFERENCE

AUTHORS

[illegible]

```

Insert Length: 16000    Std Error: 0.000
Plate: 0035    row: D    column: 08
Seq primer: GGTGTAAACACACGCGCCAT
Class: plasmid ends
High quality sequence crop: 29.
local bin/Qualifiers

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[illegible]

BASE COUNT	4 a	4 c	7 g	14 t
ORIGIN				

Category	Match	40-60	60-70	70-80	80-90	90-100	100-110	110-120	120-130	130-140	140-150	150-160	160-170	170-180	180-190	190-200	200-210	210-220	220-230	230-240	240-250	250-260	260-270	270-280	280-290	290-300	300-310	310-320	320-330	330-340	340-350	350-360	360-370	370-380	380-390	390-400	400-410	410-420	420-430	430-440	440-450	450-460	460-470	470-480	480-490	490-500	500-510	510-520	520-530	530-540	540-550	550-560	560-570	570-580	580-590	590-600	600-610	610-620	620-630	630-640	640-650	650-660	660-670	670-680	680-690	690-700	700-710	710-720	720-730	730-740	740-750	750-760	760-770	770-780	780-790	790-800	800-810	810-820	820-830	830-840	840-850	850-860	860-870	870-880	880-890	890-900	900-910	910-920	920-930	930-940	940-950	950-960	960-970	970-980	980-990	990-1000
Only Match	40-60	60-70	70-80	80-90	90-100	100-110	110-120	120-130	130-140	140-150	150-160	160-170	170-180	180-190	190-200	200-210	210-220	220-230	230-240	240-250	250-260	260-270	270-280	280-290	290-300	300-310	310-320	320-330	330-340	340-350	350-360	360-370	370-380	380-390	390-400	400-410	410-420	420-430	430-440	440-450	450-460	460-470	470-480	480-490	490-500	500-510	510-520	520-530	530-540	540-550	550-560	560-570	570-580	580-590	590-600	600-610	610-620	620-630	630-640	640-650	650-660	660-670	670-680	680-690	690-700	700-710	710-720	720-730	730-740	740-750	750-760	760-770	770-780	780-790	790-800	800-810	810-820	820-830	830-840	840-850	850-860	860-870	870-880	880-890	890-900	900-910	910-920	920-930	930-940	940-950	950-960	960-970	970-980	980-990	990-1000	
Best Local	40-60	60-70	70-80	80-90	90-100	100-110	110-120	120-130	130-140	140-150	150-160	160-170	170-180	180-190	190-200	200-210	210-220	220-230	230-240	240-250	250-260	260-270	270-280	280-290	290-300	300-310	310-320	320-330	330-340	340-350	350-360	360-370	370-380	380-390	390-400	400-410	410-420	420-430	430-440	440-450	450-460	460-470	470-480	480-490	490-500	500-510	510-520	520-530	530-540	540-550	550-560	560-570	570-580	580-590	590-600	600-610	610-620	620-630	630-640	640-650	650-660	660-670	670-680	680-690	690-700	700-710	710-720	720-730	730-740	740-750	750-760	760-770	770-780	780-790	790-800	800-810	810-820	820-830	830-840	840-850	850-860	860-870	870-880	880-890	890-900	900-910	910-920	920-930	930-940	940-950	950-960	960-970	970-980	980-990	990-1000	
Matches	15	Conservative	40-60	60-70	70-80	80-90	90-100	100-110	110-120	120-130	130-140	140-150	150-160	160-170	170-180	180-190	190-200	200-210	210-220	220-230	230-240	240-250	250-260	260-270	270-280	280-290	290-300	300-																																																																				

7 AGACACGCAAGGACCTACCA 26
 ||||| ||||| |||||
 24 AGACACGCAAGGAAATCACTA 5

RESULT 25

A2356741/

153

1. 100
 2. 100
 3. 100
 4. 100
 5. 100
 6. 100
 7. 100
 8. 100
 9. 100
 10. 100

ACCESSION

[illegible]

KEYWORDS

SOURCE

ORGANIS:

RESEARCH

12

[illegible]

ACCESSION RH793548
VERSION rh793548.1 GI:19372987
FEATURES
SOURCE fruit fly
ORGANISM Drosophila melanogaster
REFERENCE Eukaryotic Melanogaster
Neoptera: Endopterygota: Diptera: Brachycera: Muscomorpha:
Ephyra: 1 to 25
1 (bases 1 to 25)
AUTHORS Lewis, R., Hoskins, P., Li, Y. G., Morgan, N., Tsang, G., He, Y., Karpen
G., Ballou, H., Pabinger, A. and Stralinger, A.
TITLE The Berkeley Drosophila Genome Project Gene Disruption Project
JOURNAL Unpublished (2001)
COMMENT Contact: Gerald Rubin
Berkeley Drosophila Genome Project
University of California, Berkeley
LSA Building, Berkeley, CA 94720-1200, USA
Fax: 5106439447
Email: genefruity@berkeley.edu
Sequence recovery method was inverse PCR.
Sequence orientation is forward strand relative to 5' end of P
element.
The P element insertion position is base 19 in the 25 bases. This
insertion position refers to the first base of the a base target
recognition sequence.
Class: Transposon-tagged.
Location/Qualifiers
1..25
/organism="Drosophila melanogaster"
/db_xref="taxon:7227"
/clone_lib="FlyBase" cdna part P[19-25] P element
insertion lines"
/note="Inverse-PCR was performed on Drosophila
melanogaster strains each of which contains one or more
P[Super P] element. Inverse PCR was used to determine the
fragment for each strain was directly sequenced to
determine the genomic sequence at the site of insertion.
Details of the protocols used can be found at
http://www.fruityfly.org/about/methods/inverse_pcr.html."

BASE COUNT
a 7 c 8 g 7 t 7
ORIGIN
Query March 40 78, Score 12.7, DP 17, Length 75,
Best Local Similarity 62.48, Pred. No. 7.9e+05,
Matches 14, Conservative 0, Mismatches 7, Indels 0, Gaps 0

cy 1 GCGAAGATACGCTAAAC 17
|||||
25 GCGAAGATCAGCAACG 9

RESULT 19
AA66891 28 bp mRNA linear EST 13-MAR-1998
Character: Not available. Gene: Unknown IMAGE:147050.9
Similar to: P[Super P] element. FAFB:147050.9
L1 repetitive element. mRNA sequence
AA66891
AA66891 1 nt 1764167
EST
Human.
Organism Homo sapiens
Eukaryota: Metazoa: Chordata: Chordata: Vertebrata: Eumetazoa:
Mammalia: Eutheria: Primates: Catarrhini: Hominoidea: Homo
1 (bases 1 to 28)
NCI-GAP: <http://www.ncbi.nlm.nih.gov/ncbi-gap/>
National Cancer Institute, Cancer Therapy Evaluation Program (CTEP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cdaps@nci.nih.gov
Tissue Procurement: Christopher Meehan, M.D., Ph.D., Michael R.
Emmett-Ruck, M.D., Ph.D.

CDNA library preparation: M. Kent Soares, Ph.D.
CDNA library arrayed by: Greg Dench, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.S.E. Query site (URL: <http://www.fruitfly.org/seq/image.html>)
www.fruitfly.org/seq/image.html
Trace considered overall poor quality
Insert Length: 581 Std Error: 0.00
Seq primer: -40m3 fwd FT from Arabidam
High quality sequence stop: 1.
FEATURES
SOURCE
1..28
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:1457060"
/clone_lib="NCI-CGAP_Kid1"
/lab_host="DH10B"
/note="Organ. kidney. Vector: pTZ19 Pan (pharmacia) with
a modified polylinker. Site 1: Not 15 bp. Site 2: Not 15 bp.
Strand cDNA was ligated with a Not I oligo (dT) primer.
Double-stranded cDNA was ligated to Eco RI adapter
(pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pTZ19 vector.
Source: 2 pooled kidneys. Library went through one round
of normalization. Library constructed by Brent Stanton and
M. Patricia Bonaldo.
BASE COUNT
a 10 c 8 g 2 3 1 t 1
ORIGIN
Query March 40 78, Score 12.7, DP 9, Length 18,
Best Local Similarity 68.04, Pred. No. 7.9e+05,
Matches 17, Conservative 0, Mismatches 8, Indels 0, Gaps 0

cy 1 GMAAGATACGCTAAAC 26
|||||
2 GCAATACGCAAAAAAGAACACATA 26

RESULT 20
AU254545/c 29 bp mRNA linear EST 29 APR 1997
LOCUS AU254545.3
DEFINITION AU254545.3: Human cDNA library was screened with clone
P[19-25] P element.
ACCESSION AU254545
VERSION AU254545.1 GI:2614427
KEYWORDS EST.
SOURCE
house mouse.
Mus musculus.
Organism Mus musculus
Eukaryota: Metazoa: Chordata: Chordata: Vertebrata: Eumetazoa:
Mammalia: Eutheria: Rodentia: Sciurognathi: Muridae: Murinae: Mus
1 (bases 1 to 29)
Generation of expressed sequence tags from mouse brain
Unpublished (2002)
Contact: Ritsuy Kato
Graduate School of Biological Sciences
Nara Institute of Science and Technology
891-8, Takayama, Ikoma, Nara 588-8501, Japan
Tel: 81-743-72-5581
Fax: 81-743-72-5589
Email: kato@bs.nara.ac.jp
URL: <http://www.fruitfly.org/seq/image.html>
FEATURES
SOURCE
1..29
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="BEDD002430"
/clone_lib="3'-directed mouse cDNA library"
/tissue_type="brain"
/note "Vector: pTZ19"
BASE COUNT
a 9 c 4 g 5 11 t 1

BASE COUNT	1	4	7	0	6	3	10	4
ORIGIN								

Query Match	Score	Length
Best local similarity	7.78	6.42e-05
Matches	6	6
Conservative	6	6
Mismatches	6	6
Gaps	6	6

27 C GAGCAGACATCTTAAACAATCTA 28
 |||||
 34 CTGACGATTAACCAAGAGCCATCA 35

RESULT 14

AI590364

JOURNAL

unpublished

(2000)

10

[illegible]

Matches 13, Conservative 0, Mismatches 0, Inlets 0, Gaps 0

QY 3 CACAGACACCAAGACTAG 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2 CACAGACACCAAGACTAG 24

RESULT 36
US-10-098-263B-24
Sequence 264, Application US/10098263B
Publication No. US2003010010A1
GENERAL INFORMATION:
APPLICANT: Bayer, Kevin P.
APPLICANT: Bernstein, David
APPLICANT: Desmeyer, Luc
APPLICANT: Euron, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fogy, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Ashley
APPLICANT: Godowski, Paul G.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Padi, James
APPLICANT: Paoni, Nicholas P.
TITLE OF INVENTION: Secreted and Transmembrane Proteins and Related
TITLE OF INVENTION: Amino Acid Binding Site
FILE REFERENCE: P28301061
CURRENT APPLICATION NUMBER: US/10/017,407A
CURRENT FILING DATE: 2002-06-25
Prior Application removed - See File Wrapper of Padi
NUMBER OF SEQ ID NOS: 477
SEQ ID NO 294
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-10-017 407A-294

Query Match 50.8% Score 15.0 DB 15 Length 24
Best Local Similarity 79.2% Field No. 44703
Matches 18, Conservative 0, Mismatches 0, Inlets 0, Gaps 0

QY 3 CACAGACACCAAGACTAG 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2 CACAGACACCAAGACTAG 24

RESULT 37
US-10-098-263B-24248
Sequence 24248, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
Prior Application Number: 60/776,779
Prior Filing Date: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generated V 1.1
SEQ ID NO 24248
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-24248

Query Match 49.8% Score 14.8 DB 15 Length 25
Best Local Similarity 99.0% Field No. 54403
Matches 16, Conservative 0, Mismatches 0, Inlets 0, Gaps 0

QY 8 GACACCAAGACTAG 25
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 5 GACACCAAGACTAG 25

RESULT 38
US-10-098-263B-39065
Sequence 39065, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Mittman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
Prior Application Number: 60/776,779
Prior Filing Date: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 39065
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-39065

Query Match 13.3% Score 1.0 DB 15 Length 25
Best Local Similarity 92.0% Field No. 54403
Matches 16, Conservative 0, Mismatches 0, Inlets 0, Gaps 0

QY 10 CACACCAAGACTAG 27
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 3 CACACCAAGACTAG 25

RESULT 39
US-09-216-993-220
Sequence 993, Application US/09216993
Publication No. US200101447A1
GENERAL INFORMATION:
APPLICANT: Mulhausen, Michael James
TITLE OF INVENTION: TRANSFACIN-INDUCIBLE PROMOTER AND RELATED
TITLE OF INVENTION: CXC HEREOF
FILE REFERENCE: TX 1 02
CURRENT APPLICATION NUMBER: US/09/216,993
CURRENT FILING DATE: 1998-12-18
EARLIER APPLICATION NUMBER: 09/094,905
Prior Filing Date: 1997-12-19
NUMBER OF SEQ ID NOS: 364
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 220
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequences: Synthetic
OTHER INFORMATION: Primer
US-09-216-993-220

Query Match 49.8% Score 14.6 DB 15 Length 23
Best Local Similarity 81.0% Field No. 64403
Matches 17, Conservative 0, Mismatches 4, Inlets 0, Gaps 0

QY 7 AACACCAAGACTAG 27
| | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 AACACCAAGACTAG 21

RESULT 40
US-10-098-263B-81311
Sequence 81311, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:


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1 PRIOR FILING DATE: 1998-10-07
2 PRIOR APPLICATION NUMBER: 60/103315
3 PRIOR FILING DATE: 1998-10-07
4 PRIOR APPLICATION NUMBER: 60/103324
5 PRIOR FILING DATE: 1998-10-07
6 PRIOR APPLICATION NUMBER: 60/103395
7 PRIOR FILING DATE: 1998-10-07
8 PRIOR APPLICATION NUMBER: 60/103396
9 PRIOR FILING DATE: 1998-10-07
10 PRIOR APPLICATION NUMBER: 60/103401
11 PRIOR FILING DATE: 1998-10-07
12 PRIOR APPLICATION NUMBER: 60/103444
13 PRIOR FILING DATE: 1998-10-06
14 PRIOR APPLICATION NUMBER: 60/103451
15 PRIOR FILING DATE: 1998-10-08
16 PRIOR APPLICATION NUMBER: 60/103578
17 PRIOR FILING DATE: 1998-10-08
18 PRIOR APPLICATION NUMBER: 60/103711
19 PRIOR FILING DATE: 1998-10-08
20 PRIOR APPLICATION NUMBER: 60/104257
21 PRIOR FILING DATE: 1998-10-14
22 PRIOR APPLICATION NUMBER: 60/104257
23 PRIOR FILING DATE: 1998-10-20
24 PRIOR APPLICATION NUMBER: 60/105000
25 PRIOR FILING DATE: 1998-10-20
26 PRIOR APPLICATION NUMBER: 60/105002
27 PRIOR FILING DATE: 1998-10-20
28 PRIOR APPLICATION NUMBER: 60/105114
29 PRIOR FILING DATE: 1998-10-21
30 PRIOR APPLICATION NUMBER: 60/105114
31 PRIOR FILING DATE: 1998-10-22
32 PRIOR APPLICATION NUMBER: 60/105200
33 PRIOR FILING DATE: 1998-10-22
34 PRIOR APPLICATION NUMBER: 60/105200
35 PRIOR FILING DATE: 1998-10-26
36 PRIOR APPLICATION NUMBER: 60/105204
37 PRIOR FILING DATE: 1998-10-26
38 PRIOR APPLICATION NUMBER: 60/105207
39 PRIOR APPLICATION NUMBER: 60/105207
40 PRIOR APPLICATION NUMBER: 60/105207
41 PRIOR APPLICATION NUMBER: 60/105207
42 PRIOR APPLICATION NUMBER: 60/105207
43 PRIOR APPLICATION NUMBER: 60/105207
44 PRIOR APPLICATION NUMBER: 60/105207
45 PRIOR APPLICATION NUMBER: 60/105207
46 PRIOR APPLICATION NUMBER: 60/105207
47 PRIOR APPLICATION NUMBER: 60/105207
48 PRIOR APPLICATION NUMBER: 60/105207
49 PRIOR APPLICATION NUMBER: 60/105207
50 PRIOR APPLICATION NUMBER: 60/105207
51 PRIOR APPLICATION NUMBER: 60/105207
52 PRIOR APPLICATION NUMBER: 60/105207
53 PRIOR APPLICATION NUMBER: 60/105207
54 PRIOR APPLICATION NUMBER: 60/105207
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56 PRIOR APPLICATION NUMBER: 60/105207
57 PRIOR APPLICATION NUMBER: 60/105207
58 PRIOR APPLICATION NUMBER: 60/105207
59 PRIOR APPLICATION NUMBER: 60/105207
60 PRIOR APPLICATION NUMBER: 60/105207
61 PRIOR APPLICATION NUMBER: 60/105207
62 PRIOR APPLICATION NUMBER: 60/105207
63 PRIOR APPLICATION NUMBER: 60/105207
64 PRIOR APPLICATION NUMBER: 60/105207
65 PRIOR APPLICATION NUMBER: 60/105207
66 PRIOR APPLICATION NUMBER: 60/105207
67 PRIOR APPLICATION NUMBER: 60/105207
68 PRIOR APPLICATION NUMBER: 60/105207
69 PRIOR APPLICATION NUMBER: 60/105207
70 PRIOR APPLICATION NUMBER: 60/105207
71 PRIOR APPLICATION NUMBER: 60/105207
72 PRIOR APPLICATION NUMBER: 60/105207
73 PRIOR APPLICATION NUMBER: 60/105207
74 PRIOR APPLICATION NUMBER: 60/105207
75 PRIOR APPLICATION NUMBER: 60/105207
76 PRIOR APPLICATION NUMBER: 60/105207
77 PRIOR APPLICATION NUMBER: 60/105207
78 PRIOR APPLICATION NUMBER: 60/105207
79 PRIOR APPLICATION NUMBER: 60/105207
80 PRIOR APPLICATION NUMBER: 60/105207
81 PRIOR APPLICATION NUMBER: 60/105207
82 PRIOR APPLICATION NUMBER: 60/105207
83 PRIOR APPLICATION NUMBER: 60/105207
84 PRIOR APPLICATION NUMBER: 60/105207
85 PRIOR APPLICATION NUMBER: 60/105207
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94 PRIOR APPLICATION NUMBER: 60/105207
95 PRIOR APPLICATION NUMBER: 60/105207
96 PRIOR APPLICATION NUMBER: 60/105207
97 PRIOR APPLICATION NUMBER: 60/105207
98 PRIOR APPLICATION NUMBER: 60/105207
99 PRIOR APPLICATION NUMBER: 60/105207
100 PRIOR APPLICATION NUMBER: 60/105207

```

RESULT 13

```

1 US-10-006-041A 294
2 Sequence 294, Application US/1001822A
3 Publication No. US20030130490A1
4 GENERAL INFORMATION:
5 APPLICANT: Baker, Kevin P.
6 APPLICANT: Bernstein, David
7 APPLICANT: Desnoyers, Luc
8 APPLICANT: Feron, Dan I.
9 APPLICANT: Ferrara, Napoleone
10 APPLICANT: Fong, Sherman
11 APPLICANT: Gao, Wei-Qiang
12 APPLICANT: Goddard, Audrey
13 APPLICANT: Godowski, Paul J.
14 APPLICANT: Grimaldi, Christopher J.
15 APPLICANT: Gurney, Austin L.
16 APPLICANT: Hillan, Kenneth J.
17 APPLICANT: Pan, James
18 APPLICANT: Pash, Nicholas F.
19 TITLE OF INVENTION: Directed and Transmembrane Polypeptides and Nucleic
20 TITLE OF INVENTION: Acids Encoding the Same
21 FILE REFERENCE: P2810P1C
22 CURRENT APPLICATION NUMBER: US/10-006-041A

```

```

1 CURRENT FILING DATE: 2001-12-06
2 PRIOR APPLICATION REMOVED - See File Wrapper or Page
3 NUMBER OF SEQ ID NOS: 477
4 SEQ ID NO 294
5 LENGTH: 24
6 TYPE: DNA
7 ORGANISM: Artificial Sequence
8 FEATURE:
9 OTHER INFORMATION: You have selected the probe
10 US-10-006-041A 294

```

```

1 Query Match 50.0% Score 15, DB 14, Length 24
2 Best Local Similarity 78.1% Pval No. 4.4e+03
3 Matches 18, Conservative 0, Mismatches 5, Indels 0, Gaps 0

```

```

1 3 CAGAGACATCAAGACACTACG 25
2 CAGAGACATCAAGACACTACG 24

```

RESULT 14

```

1 US-10-011-813A 294
2 Sequence 294, Application US/1001822A
3 Publication No. US20030130490A1
4 GENERAL INFORMATION:
5 APPLICANT: Baker, Kevin P.
6 APPLICANT: Bernstein, David
7 APPLICANT: Desnoyers, Luc
8 APPLICANT: Feron, Dan I.
9 APPLICANT: Ferrara, Napoleone
10 APPLICANT: Fong, Sherman
11 APPLICANT: Gao, Wei-Qiang
12 APPLICANT: Goddard, Audrey
13 APPLICANT: Godowski, Paul J.
14 APPLICANT: Grimaldi, Christopher J.
15 APPLICANT: Gurney, Austin L.
16 APPLICANT: Hillan, Kenneth J.
17 APPLICANT: Pan, James
18 APPLICANT: Pash, Nicholas F.
19 TITLE OF INVENTION: Directed and Transmembrane Polypeptides and Nucleic
20 TITLE OF INVENTION: Acids Encoding the Same
21 FILE REFERENCE: P2810P1C2
22 CURRENT APPLICATION NUMBER: US/10-011-813A
23 PRIOR FILING DATE: 2002-06-25
24 PRIOR APPLICATION REMOVED - See File Wrapper or Page
25 NUMBER OF SEQ ID NOS: 477
26 SEQ ID NO 294
27 LENGTH: 24
28 TYPE: DNA
29 ORGANISM: Artificial Sequence
30 FEATURE:
31 OTHER INFORMATION: Synthetic oligonucleotide probe
32 US-10-011-813A 294

```

```

1 Query Match 50.0% Score 15, DB 14, Length 24
2 Best Local Similarity 78.1% Pval No. 4.4e+03
3 Matches 18, Conservative 0, Mismatches 5, Indels 0, Gaps 0

```

```

1 3 CAGAGACATCAAGACACTACG 25
2 CAGAGACATCAAGACACTACG 24

```

RESULT 15

```

1 US-10-015-822A 294
2 Sequence 294, Application US/1001822A
3 Publication No. US20030130490A1
4 GENERAL INFORMATION:
5 APPLICANT: Baker, Kevin P.
6 APPLICANT: Bernstein, David
7 APPLICANT: Desnoyers, Luc
8 APPLICANT: Feron, Dan I.
9 APPLICANT: Ferrara, Napoleone

```


Db 20 AGAGTACCAAGCAACCA 2

RESULT 9

US-09-864-636A-1567
 Publication No. US20030104174A1
 GENERAL INFORMATION:
 APPLICANT: Third Wave Technologies
 APPLICANT: Altmann, Halim
 APPLICANT: Pathology, Christian
 APPLICANT: Chehak, LuAnne
 TITLE OF INVENTION: Detection of RNA Sequences
 FILE REFERENCE: POPS-04944
 CURRENT AFFILIATION NUMBER: US/09/864,636A
 PRIOR FILING DATE: 2001-02-26
 NUMBER OF SEQ ID NOS: 2540
 SOFTWARE: PatentIn Version 3.0
 SEQ ID NO: 1667
 LENGTH: 10
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-864-636A-1567

Query Match 52.7% Score 15.8; DB 12; Length 30;
 Best Local Similarity 89.5% Pred. No. 2,1e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0

CY 5 AGACGACCAAGCAACCA 23
 Db 20 AGAGTACCAAGCAACCA 2

RESULT 10
 US-09-864-636A-1567
 Publication No. US20030104174A1
 GENERAL INFORMATION:
 APPLICANT: Pathology, Christian
 APPLICANT: Altmann, Halim
 APPLICANT: Pathology, Christian
 APPLICANT: Chehak, LuAnne
 TITLE OF INVENTION: Detection of RNA Sequences
 FILE REFERENCE: POPS-04944
 CURRENT AFFILIATION NUMBER: US/09/864,636A
 PRIOR FILING DATE: 2001-02-26
 NUMBER OF SEQ ID NOS: 2540
 SOFTWARE: PatentIn Version 3.0
 SEQ ID NO: 1667
 LENGTH: 10
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-09-864-636A-1567

PRIOR APPLICATION NUMBER: 60/256,402
 PRIOR FILING DATE: 2000-10-18
 PRIOR APPLICATION NUMBER: 60/271,645
 PRIOR FILING DATE: 2001-02-26
 PRIOR APPLICATION NUMBER: 60/274,809
 PRIOR FILING DATE: 2001-04-09
 PRIOR AFFILIATION NUMBER: US/09/864,636A
 PRIOR FILING DATE: 2001-03-13
 NUMBER OF SEQ ID NOS: 59
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 53
 LENGTH: 22
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence:
 OTHER INFORMATION: Nucleotide primer
 US-09-864-029-53

Query Match 50.7% Score 15.2; DB 12; Length 22;
 Best Local Similarity 85.0% Pred. No. 3.6e+04;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0

CY 10 CACGACCAAGCAACCA 29
 Db 3 CACGACCAAGCAACCA 22

RESULT 11
 US-09-864-636A-1567
 Publication No. US20030104174A1
 GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 APPLICANT: Human Microarray
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT AFFILIATION NUMBER: US/09/864,636A
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequences Mapping Generator V.1.1
 SEQ ID NO: 29595
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapien
 US-09-864-263B-29585

Query Match 50.7% Score 15.2; DB 15; Length 25;
 Best Local Similarity 85.0% Pred. No. 3.7e+03;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0

CY 5 AGACGACCAAGCAACCA 24
 Db 24 AGACGACCAAGCAACCA 25

RESULT 12
 US-09-946-374-294
 Publication No. US20030104174A1
 GENERAL INFORMATION:
 APPLICANT: Bayer, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Eisenberg, David
 APPLICANT: Batton, Dan L.
 APPLICANT: Feinberg, Stephen
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Jodanis, Andrew
 APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Christopher J.
 APPLICANT: Gurney, Austin L.

```

FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1561
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1551

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No. 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  ACGACACCAAGACACTA 23
DB      20  AAGATCACCAAGACACCA 2

RESULT 5
US-09-864-636A-1554/
Sequence 1561, Affiliation US-09-864-636A
Publication No. US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alkwal, Halim
APPLICANT: Bartholomay, Christian
APPLICANT: Chehak, LuAnne
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1554
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1554

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No. 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  ACGACACCAAGACACTA 23
DB      20  AAGATCACCAAGACACCA 2

RESULT 6
US-09-864-636A-1557/
Sequence 1557, Affiliation US-09-864-636A
Publication No. US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alkwal, Halim
APPLICANT: Bartholomay, Christian
APPLICANT: Chehak, LuAnne
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1557
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence

```

```

FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1557

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No. 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  ACGACACCAAGACACTA 23
DB      20  AAGATCACCAAGACACCA 2

RESULT 7
US-09-864-636A-1561/
Sequence 1561, Affiliation US-09-864-636A
Publication No. US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alkwal, Halim
APPLICANT: Bartholomay, Christian
APPLICANT: Chehak, LuAnne
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1561
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1561

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No. 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  ACGACACCAAGACACTA 23
DB      20  AAGATCACCAAGACACCA 2

RESULT 8
US-09-864-636A-1561/
Sequence 1561, Affiliation US-09-864-636A
Publication No. US20030104378A1
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Alkwal, Halim
APPLICANT: Bartholomay, Christian
APPLICANT: Chehak, LuAnne
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT AFFILIATION NUMBER: US-09-864-636A
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1564
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-09-864-636A-1564

Query Match      52.7%  Score 15.8  DB 12  Length 30
Best Local Similarity 89.5%  Pred No. 2.1e+03
Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      5  ACGACACCAAGACACTA 23

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C 567 11 2 47 4 29 11 US-09-890-363-3
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C 570 11 2 47 4 29 11 US-09-890-363-3
C 571 11 2 47 4 29 11 US-09-890-363-3
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C 590 11 2 47 4 29 11 US-09-890-363-3
C 591 11 2 47 4 29 11 US-09-890-363-3
C 592 11 2 47 4 29 11 US-09-890-363-3
C 593 11 2 47 4 29 11 US-09-890-363-3
C 594 11 2 47 4 29 11 US-09-890-363-3
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C 596 11 2 47 4 29 11 US-09-890-363-3
C 597 11 2 47 4 29 11 US-09-890-363-3
C 598 11 2 47 4 29 11 US-09-890-363-3
C 599 11 2 47 4 29 11 US-09-890-363-3
C 600 11 2 47 4 29 11 US-09-890-363-3

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ALIGNMENTS

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RESULT 1
US-09-890-363-3/US-09-890-363-3
Sequence 1540, Affiliation No: US-09-890-363-3
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Allway, Hakim
APPLICANT: Bartholomew, Christian
APPLICANT: Chehak, LuAnne
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1540
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Synthetic
US-09-890-363-3/US-09-890-363-3
Query Match 52.7% Score 15.81 DP 121 Length 30
Best Local Similarity 89.8% Ident 100% Mismatches 0
Matches 17 Conservative 0 Mismatches 0 Gaps 0

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Query Match 52.7% Score 15.81 DP 121 Length 30
Best Local Similarity 89.8% Ident 100% Mismatches 0
Matches 17 Conservative 0 Mismatches 0 Gaps 0

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US-09-890-363-3/US-09-890-363-3
Sequence 1540, Affiliation No: US-09-890-363-3
GENERAL INFORMATION:
APPLICANT: Third Wave Technologies
APPLICANT: Allway, Hakim
APPLICANT: Bartholomew, Christian
APPLICANT: Chehak, LuAnne
TITLE OF INVENTION: Detection of RNA Sequences
FILE REFERENCE: FORS-04944
CURRENT FILING DATE: 2002-10-15
NUMBER OF SEQ ID NOS: 2640
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1540
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Synthetic
US-09-890-363-3/US-09-890-363-3
Query Match 52.7% Score 15.81 DP 121 Length 30
Best Local Similarity 89.8% Ident 100% Mismatches 0
Matches 17 Conservative 0 Mismatches 0 Gaps 0

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[illegible]

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/261,068
 FILING DATE: 16-JUN-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Hsi, Petrina S
 REGISTRATION NUMBER: 38,496
 REFERENCE/DOCKET NUMBER: ED3
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-596-9000
 TELEFAX: 212-596-9090
 INFORMATION FOR SEQ ID NO: 16:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 34 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: unknown
 MOLECULE TYPE: rRNA
 ORIGINAL SOURCE:
 ORGANISM: Mycobacterium avium
 US-08-757-180-16

Query Match 41.38, Score 12.4, DB 1, Length 34,
 Best local Similarity 72.78, Pred. No. 8.4e+03,
 Matches 16; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 3 CAAGAGACCCAAAGACACTAC 24
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 Db 32 CAAGAGTTAAAAAGAAATTAC 11

Search completed: July 21, 2003, 15:49:05
 Job time: 32.994 secs

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492

COMPUTER PROGRAMS FILED:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: F70S/MS DOS
SOFTWARE: Patentin Release #1.0, Version #1.03
CURRENT APPLICATION DATA:

ABSTRACT NUMBER: 88/04460
FILING DATE: 31-JUN-1995

CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/761,068
FILING DATE: 16 JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/CITELI NUMBER: 1,000,001
TELEPHONE: (415) 543-9600
TELETYPE: (415) 543-5643

INFORMATION FOR SEQ. ID NO. 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
ORIGINAL SOURCE:
ORGANISM: Mycobacterium avium

FEATURES:
NAME/KEY: PREDICTED rRNA
LOCATION: 1..34
FEATURE KEY: MATCH / MISMATCH "1" = RNA "pen region"

US-08-485-602-17

Query Match: 41.3% Score: 12.4, DB: 1, Length: 34
Best Local Similarity: 70.7% From: NC_014610;
Matches: 16, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

1 CAGACGACCGCAATATATCTGC 24
|||||
1b 32 CAGACGTAAATAAATAATTTC 11

RESULT 40
US-08-757-180-16/c
Sequence 16, Application NS/08757180
Patient No. 5793201
OFFICIAL INFORMATION:
APPLICANT: Bultschaj, Theresa E
TITLE OF INVENTION: FAULTY DNA REPAIRING FOR PRELIMINARY CONTACT
TITLE OF INVENTION: FAULTY DNA REPAIRING FOR PRELIMINARY CONTACT
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSER: First & McGraw
STREET: 1251 Avenue of the Americas
City: New York
STATE: New York
COUNTRY: United States of America
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: F70S/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.03
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/06/757,180
FILING DATE: 27 May 1996
CLASSIFICATION: 435


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1 MEDIAN TYPE: floppy disk
2 COUNTRY: 1001000000
3 OPERATING SYSTEM: PC/AT/MS-DOS
4 SOFTWARE: Patent Release #1.0, Version #1.30
5
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: 05/03/2010,93A
8 FILING DATE: 10-Dec-1998
9 CLASSIFICATION: unknown
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11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: 05/03/2010,93A
13 FILING DATE: 03-Jun-1995
14 APPLICATION NUMBER: 05/03/2010,93A
15 FILING DATE: 23-Nov-1994
16
17 ACTOR/AGENT INFORMATION:
18 NAME: Brookes, A. Anders
19 REGISTRATION NUMBER: 05,773
20
21 REFERENCE/DOCID NUMBER: 05,773
22
23 TELECOMMUNICATION INFORMATION:
24 TELEPHONE: 301-309-8504
25 TELEFAX: 301-309-8439
26
27 INFORMATION FOR SEQ ID NO: 3:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 34 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
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34 MOLECULE TYPE: DNA
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REFERENCE/INVENT NUMBER: 61547-80430005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (902) 841-3000
 TELEFAX: (902) 822-6944
 TELEX: 671462JOSR
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30
 TYPE: Nucleic acid
 STRANDEDNESS: Double-stranded
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-011-22377

Query Match 42.0% Score 12.6; DB 4; Length 30;
 Best Local Similarity 78.9% Pred. No. 6.9e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 11 ACCAAGCATATTACCA 29
 DB 2 AAGAAAGAAACACCAAGAA 20

RESULT 10
 US-08-544-1818 153/C
 Sequence 153, Application US/085441818
 Patent No. 6327890
 GENERAL INFORMATION:
 APPLICANT: Cronin, Maureen T.
 APPLICANT: Miyata, Charles Guilest
 APPLICANT: Hubbell, Emil A.
 APPLICANT: Chee, Mark
 APPLICANT: Fok, Stephen P. A.
 APPLICANT: Huang, Xiaohua C.
 APPLICANT: Lipschutz, Robert J.
 APPLICANT: Lobban, Peter E.
 APPLICANT: Morris, MacDonald S.
 APPLICANT: Sheldon, Edward L.
 TITLE OF INVENTION: Arrays of Nucleic Acid Probes for
 TITLE OF INVENTION: Detecting Cystic Fibrosis
 NUMBER OF SEQUENCES: 250
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, 8th Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/544,181B
 FILING DATE: 18 OCT 1995
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/510,521
 FILING DATE: 02 AUG 1995
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/994,773
 FILING DATE: 26 OCT 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/047,064
 FILING DATE: 02 AUG 1994
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/587,432
 FILING DATE: 26 OCT 1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Lieneschuetz, Joe
 REGISTRATION NUMBER: 37,503

REFERENCE/INVENT NUMBER: 61547-80430005
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-576-0200
 TELEFAX: 415-576-0300
 INFORMATION FOR SEQ ID NO: 153:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 31 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (oligonucleotide)
 US-08-544-381B-153

Query Match 42.0% Score 12.6; DB 4; Length 31;
 Best Local Similarity 78.9% Pred. No. 6.9e+03;
 Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 4 AGAGCAACCAAGCAAT 22
 DB 28 AGAGCAACCAAGCAATTT 10

RESULT 31
 US-08-169-715-14/C
 Sequence 14, Application US/08169715
 Patent No. 6300056
 GENERAL INFORMATION:
 APPLICANT: Irvine, Bruce D.
 APPLICANT: Horn, Thomas
 APPLICANT: Chang, Chu-An
 TITLE OF INVENTION: HIV PROBES FOR USE IN SOLUTION PHASE
 TITLE OF INVENTION: SANDWICH HYBRIDIZATION ASSAYS
 NUMBER OF SEQUENCES: 63
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Morrison & Foerster
 STREET: 545 Middlefield Road, Suite 200
 CITY: Menlo Park
 STATE: California
 COUNTRY: USA
 ZIP: 94025
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/169,715
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/913,693
 FILING DATE: 18-DEC-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: Montoy, Gladys H.
 REGISTRATION NUMBER: 32,430
 REFERENCE/INVENT NUMBER: 08/000,70150.00
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 415-613-5600
 TELEFAX: 415-327-2951
 TELEX: 706141
 INFORMATION FOR SEQ ID NO: 14:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 33 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-169-715-14

Query Match 42.0% Score 12.6; DB 4; Length 33;
 Best Local Similarity 69.0% Pred. No. 6.9e+03;
 Matches 15; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

CY 2 GCAAGGACACCAAGCAATCA 26


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SOFTWARE: Word for Windows version 2.0 converted to an ASCII file
CURRENT APPLICATION DATA: US/09/487,716
APPLICATION NUMBER: US/09/487,716
FILING DATE: 10-Aug-2000
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
PRIORITY NUMBER: US/09/487,716
FILING DATE: 10-Jan-2000
APPLICATION NUMBER: US/09/487,716
FILING DATE: May 1, 1998
APPLICATION NUMBER: US/09/487,716
FILING DATE: May 1, 1998
APPLICATION NUMBER: US/09/487,716
FILING DATE: September 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Friedman, Mark M.
REGISTRATION NUMBER: 31,883
REFERENCE/DOCKET NUMBER: 4257
TELECOMMUNICATION INFORMATION:
TELEPHONE: 972 3 562553
TELEFAX: 972 3 562554
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 26
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 22
US-09-890-363-3
Query Match: 42.0%, Score: 12.6, DB: 1, Length: 26
Best Local Similarity: 42.0%, Find No. 1, Score: 12.6
Matches: 18, Conservative: 0, Mismatches: 8, Indels: 0
QY 9 AACGACAAAGACTATACG 27
DB 27 AACGACAAAGACTATACG 9
RESULT 25
US-08-592-936R 2/c
Sequence: 2, Application US/08/592,936R
Patent No. 5781393
GENERAL INFORMATION:
APPLICANT: Bestwick, Richard K.
TITLE OF INVENTION: PLANT ISSUE / STAGE SPECIFIC PROMOTERS FOR
NUMBER OF INVENTION: PERMANENT EXPRESSION OF TRANSGENES IN PLANTS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Penlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,936R
FILING DATE: 29-Jan-1996
CLASSIFICATION: 600
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4257
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
TELEPHONE: (650) 324-0960

```

```

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: RANDOM primer
US-08-592-936B 2
Query Match: 42.0%, Score: 12.6, DB: 1, Length: 30
Best Local Similarity: 42.0%, Find No. 1, Score: 12.6
Matches: 18, Conservative: 0, Mismatches: 8, Indels: 0
QY 4 AACGACAAAGACTATACGAT 30
DB 28 AACGACAAAGACTATACGCT 2
RESULT 26
US-08-788-928A-12/c
Sequence: 12, Application US/08/788,928A
Patent No. 5781394
GENERAL INFORMATION:
APPLICANT: Bestwick, Richard K.
TITLE OF INVENTION: RABBITRY PROMOTERS FOR EXPRESSION OF
NUMBER OF INVENTION: TRANSGENES IN PLANTS
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: Penlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,928A
FILING DATE: 24-Jan-1997
CLASSIFICATION: 600
TITLE APPLICATION DATA:
APPLICATION NUMBER: US 08/592,936
FILING DATE: 29-Jan-1996
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Susan T.
REGISTRATION NUMBER: 38,443
REFERENCE/DOCKET NUMBER: 4257-0015
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 324-0880
TELEFAX: (650) 324-0960
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: RANDOM primer
US 08 788-928A-12
Query Match: 42.0%, Score: 12.6, DB: 1, Length: 30
Best Local Similarity: 42.0%, Find No. 1, Score: 12.6

```

? FILING DATE: 10 JUNE 1991
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 07/030,408
 ? FILING DATE: 11-JUNE-1990
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BARRY J. SWANSON
 ? REGISTRATION NUMBER: 33,215
 ? REFERENCE/COCHET NUMBER: N/A
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (202) 793-3232
 ? TELEFAX: (202) 793-3243
 ? INFORMATION FOR SEQ ID NO: 10:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 30 base pairs
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? US-08-687-421-10

Query Match 42.7%, Score 12.8, DB 4, Length 30,
 Best Local Similarity 66.7%, Freq. No. 5, GC 63%,
 Matches 16, Conservative 1, Mismatches 7, Indels 0, Gaps 0,

CY 6 GAGATACCAATGACATACCAAT 25
 DB 6 GACCGAATGACATACCAAT 33

RESULT 22
 ? US-09-514-247A-2/c
 ? Sequence 22, Application US/0904947A
 ? Patent No. 6363161
 ? GENERAL INFORMATION:
 ? APPLICANT: TANIUCHI, TOMOYASU
 ? APPLICANT: MIZUKAMI, JUNKO
 ? TITLE OF INVENTION: METHOD FOR IDENTIFYING A SPECIFIC ANTIBODY FOR ANTIGENICITY IN HIV
 ? FILE REFERENCE: TANIUCHI-6
 ? CURRENT APPLICATION NUMBER: US/09/054,247A
 ? CURRENT FILING DATE: 2000-02-28
 ? PRIOR APPLICATION NUMBER: FFI/9826/01714
 ? PRIOR FILING DATE: 1998-08-24
 ? PRIOR APPLICATION NUMBER: FFI/1411111
 ? PRIOR FILING DATE: 1997-09-29
 ? NUMBER OF SEQ ID NOS: 10
 ? SOFTWARE: PatentIn version 3.0
 ? SEQ ID NO: 2
 ? LENGTH: 35
 ? TYPE: DNA
 ? ORGANISM: Artificial Sequence
 ? FEATURES:
 ? OTHER INFORMATION: Artificially synthesized primer sequence
 ? US-09-514-247A-2

Query Match 42.7%, Score 12.8, DB 4, Length 35,
 Best Local Similarity 70.8%, Freq. No. 1, GC 63%,
 Matches 17, Conservative 0, Mismatches 2, Indels 0, Gaps 0,

QY 7 AAAATCAATCAATCAATCAAT 49
 DB 35 AAGAGCTGAGCGACATGCAAT 12

RESULT 23
 ? US-09-260-038B-22/c
 ? Sequence 22, Application US/09067038
 ? Patent No. 6349344
 ? GENERAL INFORMATION:
 ? APPLICANT: MAY, AVAL HERBERT
 ? TITLE OF INVENTION: GENETICALLY MODIFIED CELLS AND METHODS FOR
 ? EXPRESSING RECOMBINANT HEPATITIS
 ? AND METHODS OF PURIFYING SAME
 ? NUMBER OF SEQUENCES: 25

? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Mark M. Friedman, c/o Anthony Castorina
 ? STREET: 1001 Jefferson Davis Highway, Suite 207
 ? CITY: Arlington
 ? STATE: Virginia
 ? COUNTRY: United States of America
 ? ZIP: 22202
 ? COMPUTER PROGRAM:
 ? MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
 ? COMPUTER: T4144, 31Mhz-68037
 ? OPERATING SYSTEM: MS DOS version 6.2
 ? SOFTWARE: Win32, Windows version 3.11
 ? an ASCII file

? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/260,038B
 ? FILING DATE: 02-MAR-1999
 ? CLASSIFICATION: <unknown>
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 09/041,618
 ? FILING DATE: May 1, 1998
 ? APPLICATION NUMBER: 09/071,739
 ? FILING DATE: May 1, 1998
 ? APPLICATION NUMBER: 09/022,180
 ? FILING DATE: September 2, 1997
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Friedman, Mark M.
 ? REGISTRATION NUMBER: 33,883
 ? REFERENCE/COCHET NUMBER: 310/16
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: 703-5625553
 ? TELEFAX: 703-5625554
 ? TELEX: <unknown>

? INFORMATION FOR SEQ ID NO: 22:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 29
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? US-09-260-038B-22
 ? Sequence Description: Shg 1b No: 22:

Query Match 42.7%, Score 12.4, Length 29,
 Best Local Similarity 78.9%, Freq. No. 0, GC 62%,
 Matches 15, Conservative 0, Mismatches 4, Indels 0, Gaps 0,

QY 9 AACCAAGACATACCG 27
 DB 27 ACTCCAGACATACCG 9

RESULT 24
 ? US-09-635-923-22/c
 ? Sequence 22, Application US/09063923
 ? Patent No. 6362409
 ? GENERAL INFORMATION:
 ? APPLICANT: MAY, AVAL HERBERT
 ? TITLE OF INVENTION: GENETICALLY MODIFIED CELLS AND METHODS FOR
 ? EXPRESSING RECOMBINANT HEPATITIS
 ? AND METHODS OF PURIFYING SAME
 ? NUMBER OF SEQUENCES: 25
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Mark M. Friedman c/o Anthony Castorina
 ? STREET: 1001 Jefferson Davis Highway, Suite 207
 ? CITY: Arlington
 ? STATE: Virginia
 ? COUNTRY: United States of America
 ? ZIP: 22202
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 1.44 megabyte, 3.5" microdisk
 ? OPERATING SYSTEM: MS DOS version 6.2
 ? Windows version 3.11

COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US06/714,798A
FILING DATE: 02-FEBRUARY-1996
CLASSIFICATION: 33
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/125,005
FILING DATE: 10-FEBRUARY-1994
CLASSIFICATION: 33
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/736,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/AGENT NUMBER: NEX/70
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3413
INFORMATION PER SEQ ID NO: 10
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-184-708A-10

Query Match: 42.7% Score 12.9 DB 1 Length 30
Best Local Similarity: 60.7% Pred No 5.7e-12
Matches: 16; Conservative: 1; Mismatches: 7; Indels: 0; Gaps: 0

CY 6 GAGGACGCAAGACAGACA 29
DB 6 GAGGACGCAAGACAGACA 29

RESULT 20
US-08-535-241-9
Sequence 9, Application US/05515241
Patent No. 5965551
GENERAL INFORMATION:
APPLICANT: Benoit, Patrick
APPLICANT: Denefle, Patrice
APPLICANT: Pericardet, Michel
APPLICANT: Siquet, Sandrine
APPLICANT: Vigore, Emmanuelle
TITLE OF INVENTION: RECOMBINANT VIRUSES AND THEIR USE IN
TITRE OF INVENTION: GENE THERAPY
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESS: 500 Apollo Road, 2043
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS 5.0
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09,917,243
FILING DATE: 07/09/1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/077,664/00422
FILING DATE: 15-APR-1994

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 93/05125
FILING DATE: 30-APR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, Julie Y
REGISTRATION NUMBER: 38,619
REFERENCE/AGENT NUMBER: ST/1022-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (610)424-3819
TELEFAX: (610)454-3808
INFORMATION PER SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: 30bp, 5'-GTG-3', 1120°
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-535-243-9

Query Match: 42.7% Score 12.8 DB 2 Length 30
Best Local Similarity: 47.7% Pred No 5.7e-12
Matches: 14; Conservative: 0; Mismatches: 2; Indels: 0; Gaps: 0

CY 5 AGAGACGCAAGACA 20
DB 5 AGAGACGCAAGACA 20

RESULT 21
US-08-497-421-10
Sequence 19, Application US/06497421
Patent No. 6177557
GENERAL INFORMATION:
APPLICANT: Gold, Larry
APPLICANT: Tasset, Diane
APPLICANT: Jantje, Nebojsa
TITLE OF INVENTION: HIGH AFFINITY LIGANDS OF EMBL
TITLE OF INVENTION: FIBROBLAST GROWTH FACTOR AND
NUMBER OF SEQUENCES: 445
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson & Bratschun, L.L.C.
STREET: 8400 E. Plentico Avenue, Suite 200
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/09,667,421
FILING DATE: 08-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 06/7105,095
FILING DATE: 10-FEBRUARY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 22-APRIL-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/210,912
FILING DATE: 29-MARCH-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,333
FILING DATE: 11-NOVEMBER-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131

FILING DATE: June 27, 1991
 CLASSIFICATION: 415
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US91/01822
 FILING DATE: 19 March 1991
 ATTORNEY/AGENT INFORMATION:
 NAME: John W. Caldwell
 REGISTRATION NUMBER: 28,937
 REFERENCE/AGENT NUMBER: 1515 0303
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION: SEQ ID NO. 5
 SEQUENCE CHARACTERISTICS:
 LENGTH: 26 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: other nucleic acid
 HYDROLYZABLE: NO
 ANTI SENSE: NO
 US-07-724-500B B

Query Match 41.3% Score 13 DB 1 Length 26
 Best Local Similarity 76.2% Freq No 4 76.2%
 Matches 16 Conservative 0 Mismatches 1 Indels 1

CY 2 AGAAGACACAAAGACACT 22
 |||||
 26 AGAAGACACAAAGACACT 22

RESULT 13
 US-08-547-182-4
 Sequence 4, Application US/08547182
 Patent No. 6039947
 GENERAL INFORMATION:
 APPLICANT: Campbell, Kevin P.
 APPLICANT: Lill, Leland
 APPLICANT: Duchs, Franck
 APPLICANT: Sunada, Yoshinide
 APPLICANT: Beckmann, Jacques S.
 APPLICANT: Brox, Odile
 APPLICANT: Tome, Fernando M S
 APPLICANT: Fardeau, Michel
 APPLICANT: Jackson, Charles E.
 TITLE OF INVENTION: SUBSTITUTED NUCLEIC ACID SEQUENCE
 TITLE OF INVENTION: METHODS OF MUTATIONS AND APPLICATIONS
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Kevin M. Farrell
 STREET: P.O. Box 599
 CITY: York Harbor
 STATE: ME
 COUNTRY: USA
 ZIP: 03911
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS 5.0
 SOFTWARE: Patent Release #1.0, Version #1.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/47,182
 FILING DATE:
 CLASSIFICATION: 415
 ATTORNEY/AGENT INFORMATION:
 NAME: Farrell, Kevin M.
 REGISTRATION NUMBER: 35,505
 REFERENCE/AGENT NUMBER: 1515 0303
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 207-363-0528
 TELEFAX: 207-363-0528
 INFORMATION: SEQ ID NO. 4

SEQUENCE CHARACTERISTICS:
 LENGTH: 30 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: cDNA
 US-08-547-182-4

Query Match 43.3% Score 13 DB 1 Length 30
 Best Local Similarity 76.2% Freq No 4 76.2%
 Matches 16 Conservative 0 Mismatches 5 Indels 1

CY 2 AGAAGACACAAAGACACT 22
 |||||
 26 GCAAGACACAAAGACACT 6

RESULT 14
 US-08-297-195-30
 Sequence 30, Application US/08297195A
 Patent No. 6039947
 GENERAL INFORMATION:
 APPLICANT: Howard L. Weiner
 APPLICANT: David A. Haller
 TITLE OF INVENTION: METHODS OF MUTATIONS AND APPLICATIONS
 TITLE OF INVENTION: METHODS OF MUTATIONS AND APPLICATIONS
 FILE REFERENCE: 1010/067230US3
 CURRENT APPLICATION NUMBER: US/08/297,195A
 EARLIER FILING DATE: 1994-08-11
 EARLIER APPLICATION NUMBER: 08/067,195A
 EARLIER FILING DATE: 1993-05-06
 EARLIER APPLICATION NUMBER: 07/992,559
 EARLIER FILING DATE: 1990-03-10
 EARLIER APPLICATION NUMBER: 08/005,023
 EARLIER FILING DATE: 1988-06-24
 EARLIER APPLICATION NUMBER: 07/065,734
 EARLIER FILING DATE: 1987-06-24
 NUMBER OF SEQ ID NOS: 44
 SOFTWARE: FastSeq for Windows Version 3.0
 SEQ ID NO 30
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-08-297-195-30

Query Match 43.3% Score 13 DB 3 Length 30
 Best Local Similarity 76.2% Freq No 4 76.2%
 Matches 16 Conservative 0 Mismatches 5 Indels 1

CY 2 AGAAGACACAAAGACACT 22
 |||||
 26 AGAAGACACAAAGACACT 22

RESULT 15
 5240706-19/C
 Patent No. 5240706
 APPLICANT: FAULDS, DARYL
 TITLE OF INVENTION: INTERNATIONAL ADMINISTRATION OF MICROPLASMA
 TITLE OF INVENTION: INTERNATIONAL ADMINISTRATION OF MICROPLASMA
 NUMBER OF SEQUENCES: 22
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/334,586
 FILING DATE: 07-APR-1989
 SEQ ID NO: 19
 LENGTH: 30
 5240706-19

Query Match 43.3% Score 13 DB 6 Length 30
 Best Local Similarity 76.2% Freq No 4 76.2%
 Matches 16 Conservative 0 Mismatches 5 Indels 1

CY 2 AGAAGACACAAAGACACT 22

01 11 ACCAAGACATACCTA 24
18 ATCAGACATACCTACG 1

RESULT 10
US-08-198-670A-12/C
Sequence 12, Application US/08198670A
Patent No. 5707926

GENERAL INFORMATION:
APPLICANT: GOLD, BARRY
TITLE OF INVENTION: METHOD FOR SELECTING NUCLEOTIDE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: SWANSON & BRADSHAW, L.L.C.
STREET: 3400 S. Harvard Ave., Suite 100
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch
COMPUTER: IBM PC compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: WordPerfect 6.0 for windows
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/198,670A
FILING DATE: 22 FEBRUARY-1994
CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/714,131
FILING DATE: 14 OCTOBER-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,429
FILING DATE: 11 JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,429
FILING DATE: 11 JUNE-1991

TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-198-670A-12

Query Match 44 0% Score 11.3 DB 57 Length 30
Best local similarity 52.0% Freq. No. 3.9e+04
Matches 19, Concentration 0.1 Mismatches 9, Incols 0, Baps 0

01 1 GGCAGAGACACCAACACGACGCA 26
28 GGCAGAGACACCAACACGACGCA 3

RESULT 11
PCT US93 09695 12/C
Sequence 12, Application US/0919695A
Patent No. 5707926
GENERAL INFORMATION:
APPLICANT: GOLD, BARRY M.
TITLE OF INVENTION: METHOD OF SELECTING NUCLEOTIDE
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSER: SWANSON & BRADSHAW, L.L.C.
STREET: 3400 S. Harvard Ave., Suite 100
CITY: Englewood
STATE: Colorado
COUNTRY: USA
ZIP: 80111

TITLE OF INVENTION: THE BASIS OF STRUCTURE
NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:
ADDRESSER: Beaton & Swanson, P.C.
STREET: 4582 South Uteer Street Parkway, #403
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80237

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 360 KB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/09695
FILING DATE: 12-OCT-1993
CLASSIFICATION:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/040,093
FILING DATE: 14-OCTOBER-1992
APPLICATION NUMBER: 07/714,131
FILING DATE: 10-JUNE-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/536,428
FILING DATE: 11-JUNE-1990
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 850-9900
TELEFAX: (303) 850-9401
INFORMATION FOR SEQ. ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT US93 09695 12

Query Match 44 0% Score 11.3 DB 57 Length 30
Best local similarity 52.0% Freq. No. 3.9e+04
Matches 19, Concentration 0.1 Mismatches 9, Incols 0, Baps 0

01 1 GGCAGAGACACCAACACGACGCA 26
28 GGCAGAGACACCAACACGACGCA 3

RESULT 12
US-07-124-500B-8/C
Sequence 9, Application US/0724500B
Patent No. 5736294

GENERAL INFORMATION:
APPLICANT: Becker et al.
TITLE OF INVENTION: REAGENT AND METHOD FOR MEASURING RNA EXPRESSION
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSER: MacLewicz & No. 5736294
STREET: One Liberty Place - 46th floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 MB STORAGE
COMPUTER: IBM PC/4
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/124,500B


```

FILE REFERENCE: 1948/10042
CURRENT APPLICATION NUMBER: US/09/050,100A
CURRENT FILING DATE: 1998-08-27
EARLIER FILING DATE: 1998-08-27
EARLIER APPLICATION NUMBER: 60/042,930
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 58
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence for NAME
US-09-050-159-58

Query Match      46.0%  Score 13.8  DB 4  Length 20
Best local similarity  98.2%  Pred. No. 2,1e+03
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      4  AAGAGACCAAGACCA 20
DB      19  AAGAGTACCCAGACA 3

RESULT 4
US-09-050-159-66/6
Sequence 66, Application US/09/050,100A
Patent No. 619706
GENERAL INFORMATION:
APPLICANT: No. 619706berg, Leif T
APPLICANT: Andersen, Maria K
TITLE OF INVENTION: METHODS FOR ASSESSING IMMUNOLOGICAL STATUS AND
TITLE OF INVENTION: COMPOSITIONS FOR USE THEREIN
FILE REFERENCE: 1948/10042
CURRENT APPLICATION NUMBER: US/09/050,100A
CURRENT FILING DATE: 1998-08-27
EARLIER FILING DATE: 1997-04-13/30
EARLIER APPLICATION NUMBER: 60/042,930
NUMBER OF SEQ ID NOS: 113
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 66
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence for NAME
US-09-050-159-66

Query Match      46.0%  Score 13.8  DB 4  Length 20
Best local similarity  98.2%  Pred. No. 2,1e+03
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      4  AAGAGACCAAGACCA 20
DB      19  AAGAGTACCCAGACA 3

RESULT 5
US-09-327-796 6
Sequence 6, Application US/09/050,100A
Patent No. 625512
GENERAL INFORMATION:
APPLICANT: Thiele, Mark A
APPLICANT: Mahavale, Gabriel
TITLE OF INVENTION: Regulation of Hsp-70 Expression by Cell Differentiation
TITLE OF INVENTION: By the use of Hsp-70 Messenger RNA from Cells
FILE REFERENCE: 60/050,352
CURRENT APPLICATION NUMBER: US/09/050,100A
CURRENT FILING DATE: 1999-06-08
EARLIER APPLICATION NUMBER: 60/029,233
EARLIER FILING DATE: 1998-09-04
EARLIER APPLICATION NUMBER: 60/069,491

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EARLIER FILING DATE: 1998-06-08
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patent Ver. 2.0
SEQ ID NO 6
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence for NAME
US-09-327-796-6

Query Match      46.0%  Score 13.8  DB 4  Length 20
Best local similarity  98.2%  Pred. No. 2,1e+03
Matches 15, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY      3  AAGAGACCAAGACCA 24
DB      3  AAGAGTACCCAGACA 19

RESULT 6
US-08-905-223-15
Sequence 15, Application US/08/905,223
Patent No. 622029
GENERAL INFORMATION:
APPLICANT: Edwards, Jean-Baptiste D.
APPLICANT: Lachelt, Aymeric
APPLICANT: Lachelt, Bruno
TITLE OF INVENTION: 5' Ends for JELLED Proteins
NUMBER OF SEQUENCES: 503
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kallio, Marjona, Olson & Dear
CITY: San Diego
STATE: California
COUNTRY: USA
EIL: 92101 2505
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy Disk
COMPILED: IBM PC compatible
OPERATING SYSTEM: Win95
SOFTWARE: Word
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/905,223
FILING DATE:
CLASSIFICATION: 536
ADDRESSEE/AGENT INFORMATION:
NAME: Israelson, Ned A.
REGISTRATION NUMBER: 20,655
REFERENCE/DEPOSIT NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-0176
TELEFAX: (619) 235-0550
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: Other nucleic acid
US-08-905-223-15

Query Match      43.3%  Score 13.6  DB 4  Length 29
Best local similarity  98.2%  Pred. No. 2,1e+03
Matches 16, Conservative 0, Mismatches 4, Indels 0, Gaps 0

CY      3  AAGAGACCAAGACCA 24
DB      6  AAGAGTACCCAGACA 25

RESULT 7
US-09-247-155-15

```




RESULT 40

AA33076 standard; DNA; 29 BP.

AA33076;

17 JUN 1999 (first entry)

Oligodeoxynucleotide PCR primer SEQ ID NO:15.

Human, secreted protein; EST; expressed sequence tag; diagnosis;

Hepatic, gene therapy, chemokine binding, signal peptide;

Upstream regulatory sequence, cytokine activity, cell proliferation;

differentiation, hematopoietic regulatory, tissue growth regulation;

retroactive binding regulatory, chemokine binding, hematopoietic;

chemokine, anti-inflammatory; tumor inhibition; PCR primer; SS.

Synthetic.

W0906548-A2.

11 FEB 1999.

31 JUL 1998; 98WO-1B01222.

01 AUG 1997; 97US-0905135.

(BEST) GENSET.

Duciet A, Dumas Milne Edwards C, Lacroix B;

W01; 1999-153778/13.

New nucleic acids encoding human secreted proteins - obtained from

cDNA libraries prepared from lung, liver, kidney, prostate,

kidney, lung, umbilical cord, placenta and colon tissue

Example 27; Page 45; 824pp; English.

AA33076 to AA33077 represent 5' expressed sequence tags (ESTs) for

human secreted proteins, and encode the proteins given in AA33076 to

AA33077, respectively. The proteins given represent the signal peptide

and an N-terminal fragment of a secreted protein. The nucleic acid

sequences can be used for producing secreted human gene products. They

can also be used to develop products for diagnosis and therapy. The

proteins obtained may have cytokine activity, cell

proliferation/differentiation activity, hematopoietic regulatory

activity, tissue growth regulating activity, retroviral, chemokine

regulating activity, chemokine activity, hematopoietic and

thrombolytic activity, growth, tissue activity, anti-inflammatory

activity, tumor inhibition activity or other activities. The products

can be used in forensic, gene therapy and chemokine binding procedures.

The sequences can also be used for cloning corresponding cDNA for

sequences. The nucleic acids encoding the signal peptide can be used for

directing extracellular secretion of a polypeptide or the insertion of a

polypeptide into a membrane, or inserting a polypeptide into a cell. The

present sequence represents a PCR primer used in an example from the

present invention.

Sequence 29 BP; 10 A; 8 C; 9 G; 2 T; 0 other;

Query Match 45.3%; Score 13.6; DB 20; Length 29;

Best local similarity 90.0%; Seed No. 1,00,04;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

5 AGAGACACACAGACACTAC 24

6 AGAGTCACACAGACAGACTAC 25

Search completed: July 21, 2003, 14:05:51

Job time: 119.538 secs

Query Match 45.3% Score 13.6 DB 20 Length 29
 Best Local Similarity 80.0% Seed No. 1 use 4
 Matches 16: Conservative 0: Mismatches 4: Indels 0: Gaps 0:
 5 AGAGACACCAAGAGACTAC 24
 |||||
 6 AGAGTCACGAGAGACTAC 25

RESULT 18 AAX51770

ID AAX51770 standard; DNA; 29 BP.

XX AAX51770;

XX 22 JUN 1999 (first entry)

XX Oligodeoxynucleotide primer for EST sequence.

XX Human, secreted protein, EST, expressed sequence tag, diagnosis; FCB;

XX Forensic gene therapy; chromosome mapping; signal peptide; gene;

XX differentially regulated; cytokine activity; cell proliferation;

XX reproductive hormone regulation; tissue growth regulation;

XX reproductive hormone regulation; chemokine; chemokine; hematopoietic;

XX thymolysin; cell inhibition; tumor inhibition; amplification; ss

XX Synthetic.

XX Homo sapiens.

XX W09906552-A2.

XX 11 FEB 1999.

XX 31 JUL 1998; 98WD-IB01236.

XX 01 AUG 1997; 97US-0905223.

XX (BEST) GENSET.

XX Duclert A, Dumas Milne Edwards J, Lacroix B;

XX WFI; 1999-15722713.

XX Now isolated from derived human cells - used to develop products

XX which may have cytotoxic, tumour, regulatory, haematopoietic

XX regulating, anti-inflammatory or tumour inhibition activity

XX Example 27; Page 41; 073FF; English.

XX AAX51787 to AAX52013 represent 5 expressed sequence tags (ESTs) for

XX human secreted proteins, and encode the proteins given in AAX51787 to

XX AAX52013, respectively. The proteins given represent the signal peptide

XX and an N-terminal fragment of a secreted protein. The nucleotide acids

XX sequences can be used for producing secreted human gene products. They

XX can also be used to develop a kit for diagnosis and therapy. The

XX proteins obtained may have cytokine activity, cell proliferation/

XX proliferation/differentiation activity, haematopoietic regulating

XX activity, tissue growth regulation, cytokine activity, tumour growth

XX regulating activity, chemotactic/chemokinetic activity, haematopoietic

XX activity, tumour inhibition activity or other activities. The proteins

XX can be used in forensic gene therapy and chromosome mapping procedures

XX The sequences can also be used for obtaining corresponding promoter

XX sequences. The nucleotide acids may also be used to be used for

XX detecting extracellular secretion of a polypeptide on the insertion of a

Best Local Similarity 80.0% Seed No. 1 use 4
 Matches 16: Conservative 0: Mismatches 4: Indels 0: Gaps 0:
 5 AGAGACACCAAGAGACTAC 24
 |||||
 6 AGAGTCACGAGAGACTAC 25

RESULT 39 AAX41362

ID AAX41362 standard; DNA; 29 BP.

XX AAX41362;

XX 22 JUN 1999 (first entry)

XX Oligodeoxynucleotide primer, SEQ ID NO: 15 from W09906554.

XX Human, secreted protein, EST, expressed sequence tag, diagnosis;

XX Forensic gene therapy; chromosome mapping; signal peptide; gene;

XX differentially regulated; cytokine activity; cell proliferation;

XX reproductive hormone regulation; tissue growth regulation;

XX reproductive hormone regulation; chemokine; chemokine; hematopoietic;

XX thymolysin; cell inhibition; tumor inhibition; amplification; ss

XX Synthetic.

XX Homo sapiens.

XX W09906551-A2.

XX 11-FEB-1999.

XX 31-JUL-1998; 98WD-IB01237.

XX 01-AUG-1997; 97US-0905051.

XX (BEST) GENSET.

XX Duclert A, Dumas Milne Edwards J, Lacroix B;

XX WFI; 1999-15722713.

XX Now isolated from derived human cells - used to develop products

XX cDNA libraries derived from umbilical cord, lymph ganglia,

XX lymphocytes and placental tissue

XX Example 27; Page 45; 411FF; English.

XX The patent related to sequences of 5' ESTs derived from APMs

XX encoding secreted proteins. The proteins given in AAX51787 to

XX AAX52013, respectively. The proteins given represent the signal peptide

XX and an N-terminal fragment of a secreted protein. The nucleotide acids

XX sequences can be used for producing secreted human gene products. They

XX can also be used to develop a kit for diagnosis and therapy. The

XX proteins obtained may have cytokine activity, cell proliferation/

XX proliferation/differentiation activity, haematopoietic regulating

XX activity, tissue growth regulation, cytokine activity, tumour growth

XX regulating activity, chemotactic/chemokinetic activity, haematopoietic

XX activity, tumour inhibition activity or other activities. The proteins

XX can be used in forensic gene therapy and chromosome mapping procedures

XX The sequences can also be used for obtaining corresponding promoter

XX sequences. The nucleotide acids may also be used to be used for

XX detecting extracellular secretion of a polypeptide on the insertion of a

Query Match 45.3% Score 13.6 DB 20 Length 29;

Query Match 45.3% Score 13.6 DB 20 Length 29;
 Best Local Similarity 80.0% Seed No. 1 use 4;
 Matches 16: Conservative 0: Mismatches 4: Indels 0: Gaps 0;

5 AGAGACACCAAGAGACTAC 24
 |||||
 6 AGAGTCACGAGAGACTAC 25

CC sequences. The nucleic acids encoding the signal peptide can be used for
CC directing extracellular secretion of a polypeptide. The invention of a
CC polypeptide into a molecule, or importing a polypeptide into a cell. This
CC sequence represents an oligonucleotide used in an experiment in the
CC invention, to the isolate the 5' EST sequences of the invention.

CC Sequence 2a BF, 10 A, 5 C, 2 G, 2 T, 0 other:

Query Match 45.3% Score 13.6; DB 20; Length 29;

Exact local similarity 50.0%; Identical 4; Mismatches 4; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 5 AGAGTACAGAGAGAGACTAC 24

6 AGAGTACAGAGAGAGACTAC 25

RESULT 36
AXX39423 standard; DNA; 29 BP.

AXX39423

21 JUN 1999 (first entry)

Human secreted protein 5' EST primer #3.

Human, secreted protein, EST, expressed sequence tag, diagnostic,

forensic, gene therapy, chromosome mapping, signal peptide,

secretion regulatory sequence, cytochrome P-450, cell proliferation,

differentiation, human P-450 regulation, tissue growth regulation,

regulation of human P-450, human P-450, human P-450, human P-450,

thrombolytic, anti-inflammatory, tumour inhibition; cc.

Synthetic.

WO9906550-A2.

11-FEB-1999.

31-JUL-1998; 98WO-1B01235.

01-AUG-1997; 97US-0905133.

(GEST) GENSET.

Duclet A, Dumas Milne Edwards J, Lacroix B;

WP; 1999-153761/13.

New nucleic acids encoding human secreted proteins obtained from

cDNA libraries prepared from placenta, liver, decidua, umbilical

and fetal brain tissue

Example 27, Page 40, 43pp, English.

This invention describes 5' expressed sequence tags (EST) represented

in AAX39423 to AAX3957, which encode the human secreted protein

represented in AAX39423. The proteins from secreted protein

peptide and an N-terminal fragment of a secreted protein. The nucleic

acid sequences can be used for preparing secreted protein, cell

they can also be used to detect a secreted protein. The

protein obtained may have cytochrome P-450, cell

proliferation, differentiation, cell growth, cell

activity, tissue growth, regulatory activity, cell

regulating activity, cytochrome P-450, cell

thrombolytic activity, human P-450, cell

activity, human P-450, cell growth, cell

can be used to detect a secreted protein and the

The sequence can also be used for identifying

sequences. The nucleic acids encoding the signal

directing extracellular secretion of a polypeptide

polypeptide into a membrane, or importing a

CC sequence represented a primer which is used in the method of the

CC invention.

CC Sequence 2a BF, 10 A, 5 C, 2 G, 2 T, 0 other:

Query Match 45.3% Score 13.6; DB 20; Length 29;

Exact local similarity 50.0%; Identical 4; Mismatches 4; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Db 5 AGAGTACAGAGAGAGACTAC 24

6 AGAGTACAGAGAGAGACTAC 25

RESULT 37
AAX40421

ID AAX40421 standard; DNA; 29 BP.

AAX40421

18-JUN-1999 (first entry)

Seq ID No:15 of WO9906550.

Human, secreted protein, EST, expressed sequence tag, diagnostic,

forensic, gene therapy, chromosome mapping, signal peptide,

secretion regulatory sequence, cytochrome P-450, cell proliferation,

differentiation, human P-450 regulation, tissue growth regulation,

regulation of human P-450, human P-450, human P-450, human P-450,

thrombolytic, anti-inflammatory, tumour inhibition; cc.

Synthetic.

WO9906550-A2.

11-FEB-1999.

31-JUL-1998; 98WO-1B01232.

01-AUG-1997; 97US-0905144.

(GEST) GENSET.

Duclet A, Dumas Milne Edwards J, Lacroix B;

WP; 1999-153760/13.

New isolated prostate-derived nucleic acids - used to develop

products which may have cytochrome P-450, cell

regulating, anti-inflammatory or tumour inhibition activity

Example 27, Page 40, 43pp, English.

AAX40421 to AAX40425 represent 5' expressed sequence tags (EST) for

human secreted proteins expressed in prostate, and encode the proteins

given in AAX40421 to AAX40425 respectively. The proteins given represent

the signal peptide and an N-terminal fragment of a secreted protein. The

nucleic acid sequences can be used for preparing secreted protein, cell

they can also be used to detect a secreted protein. The

protein obtained may have cytochrome P-450, cell

proliferation, differentiation, cell growth, cell

activity, tissue growth, regulatory activity, cell

regulating activity, cytochrome P-450, cell

thrombolytic activity, human P-450, cell

activity, human P-450, cell growth, cell

can be used to detect a secreted protein and the

The sequence can also be used for identifying

sequences. The nucleic acids encoding the signal

directing extracellular secretion of a polypeptide

polypeptide into a membrane, or importing a

WP1: 1999-347470/20
 XX Extended clones encoding secreted proteins
 XX Example 27, Page 143, 1999, English.
 XX This invention relates to novel amino acid sequences of extended clones
 CC (see AAX51442) which encode human secreted proteins (see
 CC AAX51442) and which have cytotoxic, chemotherapeutic and cytotoxic
 CC activity. The extended clones can be used to express secreted proteins
 CC or parts of them or to obtain antibodies capable of binding to the
 CC secreted proteins. They may also be used in diagnostic, forensic,
 CC gene therapy, and gene therapy applications. They also include design
 CC of expression vectors and secretion vectors. This sequence represents
 CC a PCR primer used in the method of the invention.
 XX
 XX Sequence 29 BP: 10 A, 4 C, 9 G, 2 T, 0 other:

Query March 45 38 Score 13.6 DB 20 Length 29
 Blast local similarity 80.081 Pred. No. 1.9e+04
 Matches 16 Conserved 0 Mismatches 4 Indels 0 Gaps 0

5 AGAGACACGACAAAGACACTAC 24
 |||||
 6 AGAGACACGACAAAGACACTAC 25

RESULT 34
 ID AAX51442 standard, DNA, 29 BP.
 XX
 XX AAX51442:
 XX
 XX 13-SEP-1999 (first entry)
 XX
 XX PCR primer for extended secreted protein coding sequences.

XX Secreted protein; human; cytokine; cellular proliferation; anti-tumor;
 XX cellular differentiation; immune system regulator; anti-inflammatory;
 XX hematopoietic regulator; tissue growth regulator; tumor inhibitor;
 XX reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 XX genetic disease; PCR primer; ss.
 XX
 XX Synthetic.
 XX Homo sapiens
 XX
 XX W09031236 A7
 XX
 XX 24-JUN-1999.
 XX
 XX 17-DEC-1998; 98MO 1802122.
 XX
 XX 10-AUG-1998; 98US 0066116.
 XX 17-DEC-1997; 97US 0069957.
 XX 09-FEB-1998; 98US 0074121.
 XX 13-APR-1998; 98US 0081583.
 XX
 XX (GIST) GENSET.

XX Bouquollet L, Duclert A, Dumas Milne Edwards J.
 XX
 XX W071 1333 1999/33.
 XX
 XX How induced human secreted proteins
 XX
 XX Example 27, Page 143, 1999, English.

XX This sequence represents a PCR primer used in the isolation of the
 CC extended human secreted protein coding sequences (see the invention). The
 CC extended clones can be used to express secreted proteins or parts of
 CC human secreted proteins. They may also be used in diagnostic, forensic,
 CC gene therapy, and gene therapy applications. They also include design
 CC of expression vectors and secretion vectors. This sequence represents
 CC a PCR primer used in the method of the invention.

XX secreted protein; human; cytokine; cellular proliferation; anti-tumor;
 CC chemotactic/chemotaxis; immune system regulator; anti-inflammatory;
 CC inhibition activity. The clones can be used in forensic procedures to
 CC identify individuals or in diagnostic procedures to identify individuals
 CC having genetic disease. They may also be used in diagnostic, forensic,
 CC gene therapy, and gene therapy applications. They also include design
 CC of expression vectors and secretion vectors. This sequence represents
 CC a PCR primer used in the method of the invention.

Query March 45 38 Score 13.6 DB 20 Length 29
 Blast local similarity 80.081 Pred. No. 1.9e+04
 Matches 16 Conserved 0 Mismatches 4 Indels 0 Gaps 0

5 AGAGACACGACAAAGACACTAC 24
 |||||
 6 AGAGACACGACAAAGACACTAC 25

RESULT 35
 ID AAX51442 standard, DNA, 29 BP.
 XX
 XX AAX51442:
 XX
 XX 21-JUN-1999 (first entry)
 XX
 XX PCR primer for 5' EST sequence.

XX Human; secreted protein; EST; expressed sequence tag; diagnostic;
 XX forensic; gene therapy; chemotactic/chemotaxis; immune system
 XX regulator; cytokine; cellular proliferation; anti-tumor;
 XX hematopoietic regulator; tissue growth regulator; tumor inhibitor;
 XX reproductive hormone regulator; chemotaxis; chemokinesis; gene therapy;
 XX genetic disease; PCR primer; ss.
 XX
 XX Synthetic.
 XX Homo sapiens
 XX
 XX W09090540 A2.
 XX
 XX 11-FEB-1999.
 XX
 XX 31-JUL-1998; 98MO 1801231.
 XX 01-AUG-1997; 97US 0066279.
 XX
 XX (GIST) GENSET.

XX Duclert A, Dumas Milne Edwards J, Macroix B.
 XX
 XX W071 1333 1999/33.
 XX
 XX New nucleic acids encoding human secreted proteins obtained from
 CC cDNA libraries derived from testis, ovary, uterus and spleen tissue
 XX
 XX Example 27, Page 143, 1999, English.

XX AAX51459 to AAX51601 represent 5' expressed sequence tags (ESTs) for
 CC human secreted proteins, and encode the proteins given in AAX51459 to
 CC AAX51601. The proteins given represent the normal amino acid
 CC and an internal fragment of a secreted protein. The nucleic acid
 CC sequences can be used for predicting secreted human gene products. They
 CC can also be used to develop probes for diagnostic and therapy. The
 CC proteins obtained may have cytokine activity, hematopoietic regulator
 CC activity, tissue growth regulator activity, anti-tumor activity, immu-
 CC noregulatory activity, chemotactic/chemotaxis activity, hematopoietic
 CC and hematopoietic activity, reproductive hormone activity, and inflammatory
 CC activity. They may also be used in diagnostic, forensic, gene therapy,
 CC and gene therapy applications. They also include design
 CC of expression vectors and secretion vectors. This sequence represents
 CC a PCR primer used in the method of the invention.

OS	Mus sp.
XX	
PN	W0200107081 A1.
XX	
PD	01-FEB-2001.
XX	
PE	21 JUL-2000; 2000MO US19816
XX	
PR	21-JUL-1999; 99US-0144965.
XX	
FA	(LEXI) LEXIGEN PHARM CORP
XX	
P1	Gillies SD, de RM, Woodhouse CO,
XX	
DR	WDJ; 2001 1972R/1R
XX	
FT	Abstracts are for abstracting the immunogenicity of protein and peptide antigens, comprise F-fusion proteins, or F antigen fusion proteins or Fc adjuvant fusion proteins.
PT	
XX	
PS	Example 1; Page 10; 78pp; English.
XX	
CC	The present invention relates to compositions for eliciting an enhanced immune response against a preselected antigen. The compositions comprise a fusion protein with an immunoglobulin heavy chain constant region linked by a polypeptide linker to an antigenic epitope. In one aspect, the invention provides a nucleotide sequence encoding the fusion protein, where expression results in the production of the fusion protein. The present sequence is a PCR primer used in the present invention to amplify the antigen expression gene.
SC	Sequence: GA BP; 3 A; 6 G; 3 G; 7 T; 0 other;
XX	
Query Match:	46.0%; Comp: 13.9; FR: 0.0; Length: 29.
Best Local Similarity:	72.0%; Fred: NO; 1.6e+04;
Matches:	1st: conservative; 2nd: Moderate; 3rd: Identity; 4th: Gap; 5th: Mismatch
QY	3 CAGACATCTCCTAAACACTGTCATCAT 27 DB 28 CTGAGACTGGGAATCACTCCTACCTG 4
RESULT 30	
ID	AHA99127/c
XX	
SD	AHA99127 standard; DNA; 28 BP.
XX	
AF	AHA99127;
XX	
DT	19-JUN-2002 (first entry)
XX	
DE	Primer #1 used to isolate the F19 encoding nucleotid will sequence
XX	
KM	Antibody: anti-mouse IgG, purified, anti-HIV, seq. Immunogen: HIV, pep primer: p16
XX	
OS	Synthetic.
XX	
FN	W02000202143-A2.
XX	
P2	10-JAN-2002.
XX	
PF	29-JUN-2001; 2001WO-US2095R.
XX	
PR	29 JUN 2000; 2000US 215318F.
XX	
PA	(LEXI-) LEXIGEN PHARM CORP
XX	
P1	Gillies SD, Lee Y, Hulten SA;
XX	
DP	WDJ; 2002 164499/71
XX	
TI	Inducing cytotoxic T lymphocyte responses against tumour in mammals by

PT administering immunocytokine, and immunocytokine of the enhanced agent
PT that enhances immune response induced by the immunocytokine.
XX
PS Example 2; Page 25; 4pp; English.

This invention relates to inducing a cytotoxic immune response against
CC a tumor in a mammal, by the administration of an immunocytokine
CC comprising an antibody binding site and an immunocytokine of the
CC enhancing agent. The method is embodied and illustrated, cytotoxic
CC vincristine, and anti-HIV in its action. The method is useful for
CC treating certain viral diseases where an immune suppressive mechanism
CC prevents effective cellular immunity e.g., liver metastatic melanoma virus
CC (HIV) infection. It is also useful for treating tumor and other
CC cancerous or diseased cells, and in mediating immune destruction of
CC virus infected cells. Administration of immunocytokine with
CC enhancing agent increases a more potent antitumor response since the
CC enhancing agent increases or enhances the therapeutic effect of the
CC antibody-cytokine factor resulting in increasing or increasing its effect
CC by the tumor. The immunocytokine operates enhancing agent increases the
CC penetration of immunocytokine into the tumor micro environment thus
CC making it capable of overcoming the immune suppressive effect and to
CC effective at activating cellular responses within the tumor. The
CC combined therapy is effective in mediating the immune destruction of a
CC diseased tissue. Therefore, a lower dosage of the chemotherapeutic agent
CC may be administered to a patient, thus suppression of a patient's immune
CC system often associated with treatment using chemotherapy agent is
CC reduced. This subject represents a primer used to isolate the p6
CC encoding nucleic acid sequence which also adapted to the p6 as an
CC XbaI-XhoI restriction fragment.

Sequence: 79 AT, 3 A, 3 G, 9 G, 7 T, 0 other;

Query Match 48.8%; Score 13.9; E-24; Length 24;
Best Local Similarity 72.0%; Pred. No. 1.6e+04;
Matches: 29, Conservative 9, Miscellaneous 7, Indels 0, Gaps 0

3 CAAAGACATCTATTAAAGCAACTACGAG 27
||||| |||||
28 CAAAGACATCTAAATGAAGTACCGC 4

RESULT 31
ABK68316/c
ID ABK68316 standard; DNA; 25 BP.
AC
ABK68316;
XX
XX 27 AUG-2002 (first entry)
ET
XX
XX Mouse TGR346b RACE primer #1.
DE
XX
XX Mouse TGR346b (RACE); ss. 3'-flank coupled receptor (GPCR); TR; P/B
XX TGR-associated disorder; signal transduction; renal failure; nephritis;
XX hyperphosphatemia; hypocalcemia; calcinosis; proteinuria; heart failure;
XX tubercle; osteitis; hyperostosis; osteoarthritis; distal distal artery disease;
XX sleep disturbance; temperature regulation; blood pressure; hyperhidrosis;
XX circadian rhythm; RACE.
XX
OS Mus sp.
XX
XX W0000942459 AC.
PI
XX
XX 30-MAY-2002.
PD
XX
XX 21 NOV-2001, 2001MO-US43404.
TF
XX
XX 22-NOV-2000; 2000MS-252841P
PR 20-DEC-2000; 2000MS-267834P
PR 10-JAN-2001; 2001MS-261377P
PR 29 MAR-2001; 2001MS-279554P
PR 29 MAR-2001; 2001MS-280596P
XX
XX (TGA.) TUNAFIR INC.

Matches 16, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY 8 GACAGCAAGACACTAC 24
 |||||
 DB 4 GACAGCAAGACACTAC 20

RESULT 27

AA220897/c
 ID AA220897 standard, 28 BP.

XX
 XX
 AC AA220897

XX 31-JAN-2000 (first entry)

DE Murine IL-12 subunit p35 cDNA amplifying primer.

XX
 KW Cytokine, immunoregulatory, gamma 12, murine response against tumor,
 KW pleiotropic inhibitor of HIV infection; HIV infection;
 KW K2 antigen, fusion protein, interaction, 10, 10, PCR primer, 20.

XX
 OS Synthetic.

OS Mus sp.

XX W09952562-A2.

XX 28-OCT-1999.

PF 16-APR-1999; 99W0-US08176

XX 17-APR-1998; 98US-0082166.

XX (LEXI-) LEXIGEN PHARM CORP.

XX Gillies SD;

XX WPI, 1999 022008/4

XX Combining heavy for enhanced gamma 12 response to HIV infection;
 PT cancer and virus-infected cells

XX
 PO Example 2, Page 23, 50th, English

XX The invention relates to a method to enhance an antibody response

XX immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

ID AA220897 standard, 28 BP.

XX
 AC AA220897

XX 28 JAN-2000 (first entry)

DE PCR primer used to amplify cDNA encoding murine p35 interleukin 12

XX PCR primer: human K5 antigen; EPCAM; murine gamma2a interferon 12

XX Cytokine, immunoregulatory, gamma 12, murine response against tumor,
 KW pleiotropic inhibitor of HIV infection; HIV infection;
 KW K2 antigen, fusion protein, interaction, 10, 10, PCR primer, 20.

XX solid tumour; ss.

XX
 OS Synthetic.

OS Mus sp.

XX W09952562-A2.

XX 28 OCT-1999.

PF 15-APR-1999; 99W0-US08176.

XX 15-APR-1998; 98US-0081863.

XX (LEXI-) LEXIGEN PHARM CORP.

XX Gillies SD;

XX WPI, 1999 022008/4.

XX Novel method of inducing a cytotoxic immune response against
 PT virus-infected cells using a specific antibody

XX Example 2, Page 26, 48th, English.

XX PCR primers AA220897-03 were used to amplify cDNA encoding murine p35

XX interleukin 12 (IL-12) subunit, which was used to construct a
 CC encoding a human K5 antigen (K5A or EPCAM) murine gamma2a interferon 12

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX The present invention relates to a method of using a specific
 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

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 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

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 CC cell-type in a murine system, by a method of using a specific

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 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

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 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

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 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

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 CC cell-type in a murine system, by a method of using a specific

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 CC cell-type in a murine system, by a method of using a specific

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 CC cell-type in a murine system, by a method of using a specific

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 CC cell-type in a murine system, by a method of using a specific

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 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

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 CC cell-type in a murine system, by a method of using a specific

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 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

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 CC immunoregulatory induced by gamma 12, murine response against tumor,
 CC cell-type in a murine system, by a method of using a specific

XX wt; 1989-06/27/94.

XX

PT Multiple strand displacement amplification

XX

PC Example 1, Page 38, 57P, English.

CC [Abstract] Reference primers used for multiple strand displacement
amplification include DNA template, the method of invention,
CC primers having at least one primer, and primer extension
reference light primers. The specification describes a method for
CC amplification of specific target acids using strand displacement.
CC replication of nucleic acid sequences by multiple primers in a
CC continuous isothermal reaction. The method, termed multiple strand
displacement amplification (MSDA), or whole genome strand displacement
amplification (WGSDA) is useful for amplification of nucleic acids
and where genomic DNA is used as a template for RNA expression profiling.

SQ Sequence 19 BP; 3 A; 3 C; 4 G; 9 T; 0 other;

DY Daily March, 1989, Scale 1:4, FR 75 Length 19;
Best local similarity: 23.6%, final score +0.3;
Method: BL, threshold = 0, mismatches: 1; inserts: 0; gaps:
0

SA 9 GAGATGAAAGACACTTA 73
|||||
||| | |||||
16 AGCAAGAACAAAAATA 3

RESULT 11
AB000310C
ID AB000912 standard; DNA; 24 BP.
XX AR000912/
XX AC AR000912/
DT 11-JUN 2002 (first entry)
SE 03-NOV-2001 219-1109-11:12 84X.
XX
XX Oligonucleotide array; adapter sequence; probe; ss.
OS Synthetic.
XX
XX EN WO200216649-A2.
PN 28-FEB-2002.
XX
XX 27-MAR-2002, 2001WO 026019.
FR 26 AUG 2003; 2000US 227949P.
FR 29 AUG 2003; 2000US 229854P.
XX
XX PA (ILUC-) ILLUMINA INC.
PA Gunderson K,
XX
XX WI; 2002-09/26/94.
XX
XX Array comprising adapted sequences useful for immobilizing or detecting
a target nucleic acid sequence, has different addresses consisting
of different specific capture probes -
XX
PS Claim 1, Page 63, 26pp; English.

CC The invention relates to an oligonucleotide array (I) comprising at least
25 different addresses (adapter sequences) with each comprising a
CC different sequence (probe). From a group consisting of the sequences
given in SEQ ID NO: 1-14, (II) is useful for immobilising a target
CC nucleic acid sequence by attaching a adapter nucleic acid
(SEQ ID NO: 15-30) to a target nucleic acid to form a modified target
CC nucleic acid and contacting the modified target nucleic acid with reagent
CC the steps of above method is useful for detecting a target nucleic acid,
which further comprises detecting the presence of the modified target

XX DBP1: 1997-0097/11/01.
 XX
 PT New vector containing an insert coding a hybrid protein with
 PT domains for binding and effector function - used in
 PT transfecting/transducing mammalian cells in treating diseases where
 PT cell migration and/or tissue remodeling occurs
 XX
 PS Example 3, Page 3, 39ff, English.
 XX
 CC Sequence AAV33933 & AAV33934 represent primers used in the construction
 CC of the plasmids of the invention. The invention provides a recombinant
 CC nucleic acid molecule, comprising a vector containing an insertion
 CC encoding an effector hybrid protein, a binding domain and a
 CC with binding/effector function, used for transfecting/transducing
 CC mammalian cells. The vector is made up of a
 CC protein coding region, a binding domain, a binding domain, a
 CC insertion and tissue remodeling, through transfection/transduction in
 CC out of their environment with the vector. In order to obtain local
 CC expression of the hybrid protein, the vector, in addition to the local
 CC enables a process for producing hybrid protein, which are
 CC expressed following transfection/transduction in the cells, which are
 CC selective recovery. The processes are useful in treating diseases in
 CC which cell migration and/or tissue remodeling occurs. The vector and the
 CC local expression of a protein inhibitor that binds to a specific
 CC receptor at the cell surface, so it can inhibit protein by its action
 CC bound to receptors, or prevent them from binding.
 XX
 SO Sequence 25 BP: 11 A; 8 C; 5 G; 1 T; 0 other:
 Query Match 52.0%, Score 15.6; DB 20; Length 25;
 Best Local Similarity 81.8%, Field No. 236+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 5 AAGACACCAAGACACTACCA 26
 DB 3 AAGACACCAAGACACTACCA 24
 RESULT 3
 AAV33933
 ID AAV33933 standard; DNM; 25 BP.
 XX
 AC AAV33933;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Human TIMP1 cDNA amplifying primer for constructing plasmid pGEM1 TIMP1.
 XX
 KW Recombinant hybrid protein, binding effector function, transfection,
 KW transfection, hybrid protein, binding effector function, transfection,
 KW cell migration, tissue remodeling, protein inhibitor, pGEM1 TIMP1,
 KW human tissue inhibitor of metalloproteinases, TIMP1, PCF primer, etc.
 XX
 OS Synthetic
 OS Homo sapiens.
 XX
 FN W09071700 A2
 XX
 PD 19-NOV-1998.
 XX
 PF 11-MAY-1998; 98WO-NL000294.
 XX
 PR 12-MAY-1997; 97EF-0001423.
 XX
 PA (NEDE) NEDERLANDSE ORG TOEGEPAST.
 XX
 XX Quax PMA, Verheijen JM,
 XX
 DR WPI: 1997-0097/11/01
 XX
 PT New vector containing an insert coding a hybrid protein with
 PT domains for binding and effector function - used in

PT transfecting/transducing mammalian cells in treating diseases where
 PT cell migration and/or tissue remodeling occurs
 XX
 PS Example 6, Page 13, 39ff, English.
 XX
 CC Sequence AAV33933 & AAV33934 represent primers used in the construction
 CC of the plasmids of the invention. The invention provides a recombinant
 CC nucleic acid molecule, comprising a vector containing an insertion
 CC encoding an effector hybrid protein, a binding domain and a
 CC with binding/effector function, used for transfecting/transducing
 CC mammalian cells. The vector is made up of a
 CC protein coding region, a binding domain, a binding domain, a
 CC insertion and tissue remodeling, through transfection/transduction in
 CC out of their environment with the vector. In order to obtain local
 CC expression of the hybrid protein, the vector, in addition to the local
 CC enables a process for producing hybrid protein, which are
 CC expressed following transfection/transduction in the cells, which are
 CC selective recovery. The processes are useful in treating diseases in
 CC which cell migration and/or tissue remodeling occurs. The vector and the
 CC local expression of a protein inhibitor that binds to a specific
 CC receptor at the cell surface, so it can inhibit protein by its action
 CC bound to receptors, or prevent them from binding.
 XX
 SO Sequence 25 BP: 11 A; 8 C; 5 G; 1 T; 0 other:
 Query Match 52.0%, Score 15.6; DB 20; Length 25;
 Best Local Similarity 81.8%, Field No. 236+03;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 OY 5 AAGACACCAAGACACTACCA 26
 DB 3 AAGACACCAAGACACTACCA 24
 RESULT 4
 AAV33933
 ID AAV33933 standard; DNM; 25 BP.
 XX
 AC AAV33933;
 XX
 DT 26-MAR-2002 (first entry)
 XX
 DE Human G protein-coupled receptor, GPCR4, reverse PCR primer, AAV33933.
 XX
 KW Human, ss, GPCR4, G protein-coupled receptor, developmental disorder,
 KW immune disease, taste and scent detectability disorder,
 KW Burkitt's lymphoma, signal transduction pathway disorder,
 KW renal disease, renal growth rate disorder, feeding disorder,
 KW congenital deafness, hearing, strabismus, fungal infection,
 KW neuroblastoma, depression, diabetes mellitus, bacterial infection,
 KW fibrous dysplasia, viral infection, fibrous dysplasia, fibrous
 KW (Albright) Parry-Romberg disease, acute lymphatic leukaemia, hypoparathyroidism,
 KW hypoparathyroidism, urinary retention, osteoporosis, Crohn's disease,
 KW multiple sclerosis, Alagille hereditary, osteoporosis, anemia, psychosis,
 KW myocardial infarction, diabetes mellitus, benign prostatic hyperplasia,
 KW manic depression, delirium, dementia, severe mental retardation,
 KW autoimmune dominant (2) Autosomal recessive, dyslipidemia, for protein,
 KW Huntington's disease, stroke, de la Tourette syndrome, Alagille
 KW haemorrhagic disorder, cell signal processing disorder,
 KW metabolic pathway modulation disorder.
 XX
 OS Homo sapiens.
 XX
 FN W0200190187-A2.
 XX
 PD 29-NOV-2001.
 XX
 PF 24-MAY-2001; 2001WO-0517114.
 XX
 PR 24-MAY-2001; 2001WO-0517114.
 XX
 PA 24-MAY-2001; 2001WO-0517114.
 XX
 XX 24-MAY-2001; 2001WO-0517114.
 XX
 DR WPI: 1997-0097/11/01
 XX
 PT New vector containing an insert coding a hybrid protein with
 PT domains for binding and effector function - used in

521	11.6	38.7	30	20	AAV9196	Human tumour antigen
522	11.6	39.7	30	20	AAV9197	Human tumour antigen
523	11.6	39.7	30	20	AAV9198	Human tumour antigen
524	11.6	39.7	30	20	AAV9199	Human tumour antigen
525	11.6	39.7	30	20	AAV9200	Human tumour antigen
526	11.6	39.7	30	20	AAV9201	Human tumour antigen
527	11.6	39.7	30	20	AAV9202	Human tumour antigen
528	11.6	39.7	30	20	AAV9203	Human tumour antigen
529	11.6	39.7	30	20	AAV9204	Human tumour antigen
530	11.6	39.7	30	20	AAV9205	Human tumour antigen
531	11.6	39.7	30	20	AAV9206	Human tumour antigen
532	11.6	39.7	30	20	AAV9207	Human tumour antigen
533	11.6	39.7	30	20	AAV9208	Human tumour antigen
534	11.6	39.7	30	20	AAV9209	Human tumour antigen
535	11.6	39.7	30	20	AAV9210	Human tumour antigen
536	11.6	39.7	30	20	AAV9211	Human tumour antigen
537	11.6	39.7	30	20	AAV9212	Human tumour antigen
538	11.6	39.7	30	20	AAV9213	Human tumour antigen
539	11.6	39.7	30	20	AAV9214	Human tumour antigen
540	11.6	39.7	30	20	AAV9215	Human tumour antigen
541	11.6	39.7	30	20	AAV9216	Human tumour antigen
542	11.6	39.7	30	20	AAV9217	Human tumour antigen
543	11.6	39.7	30	20	AAV9218	Human tumour antigen
544	11.6	39.7	30	20	AAV9219	Human tumour antigen
545	11.6	39.7	30	20	AAV9220	Human tumour antigen
546	11.6	39.7	30	20	AAV9221	Human tumour antigen
547	11.6	39.7	30	20	AAV9222	Human tumour antigen
548	11.6	39.7	30	20	AAV9223	Human tumour antigen
549	11.6	39.7	30	20	AAV9224	Human tumour antigen
550	11.6	39.7	30	20	AAV9225	Human tumour antigen
551	11.6	39.7	30	20	AAV9226	Human tumour antigen
552	11.6	39.7	30	20	AAV9227	Human tumour antigen
553	11.6	39.7	30	20	AAV9228	Human tumour antigen
554	11.6	39.7	30	20	AAV9229	Human tumour antigen
555	11.6	39.7	30	20	AAV9230	Human tumour antigen
556	11.6	39.7	30	20	AAV9231	Human tumour antigen
557	11.6	39.7	30	20	AAV9232	Human tumour antigen
558	11.6	39.7	30	20	AAV9233	Human tumour antigen
559	11.6	39.7	30	20	AAV9234	Human tumour antigen
560	11.6	39.7	30	20	AAV9235	Human tumour antigen
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563	11.6	39.7	30	20	AAV9238	Human tumour antigen
564	11.6	39.7	30	20	AAV9239	Human tumour antigen
565	11.6	39.7	30	20	AAV9240	Human tumour antigen
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570	11.6	39.7	30	20	AAV9245	Human tumour antigen
571	11.6	39.7	30	20	AAV9246	Human tumour antigen
572	11.6	39.7	30	20	AAV9247	Human tumour antigen
573	11.6	39.7	30	20	AAV9248	Human tumour antigen
574	11.6	39.7	30	20	AAV9249	Human tumour antigen
575	11.6	39.7	30	20	AAV9250	Human tumour antigen
576	11.6	39.7	30	20	AAV9251	Human tumour antigen
577	11.6	39.7	30	20	AAV9252	Human tumour antigen
578	11.6	39.7	30	20	AAV9253	Human tumour antigen
579	11.6	39.7	30	20	AAV9254	Human tumour antigen
580	11.6	39.7	30	20	AAV9255	Human tumour antigen
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582	11.6	39.7	30	20	AAV9257	Human tumour antigen
583	11.6	39.7	30	20	AAV9258	Human tumour antigen
584	11.6	39.7	30	20	AAV9259	Human tumour antigen
585	11.6	39.7	30	20	AAV9260	Human tumour antigen
586	11.6	39.7	30	20	AAV9261	Human tumour antigen
587	11.6	39.7	30	20	AAV9262	Human tumour antigen
588	11.6	39.7	30	20	AAV9263	Human tumour antigen
589	11.6	39.7	30	20	AAV9264	Human tumour antigen
590	11.6	39.7	30	20	AAV9265	Human tumour antigen
591	11.6	39.7	30	20	AAV9266	Human tumour antigen
592	11.6	39.7	30	20	AAV9267	Human tumour antigen
593	11.6	39.7	30	20	AAV9268	Human tumour antigen



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Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY
6 GAGACACCAAGACATACGACA 29
|||
28 GATACACCATACGACATACGACA 5
RESULT 39
A40277      30 bp      DNA      linear      FAT 05 MAR-1997
DEFINITION
Sequence 9 from Patent WO9425073.
A40277
A40277.1  GI:2206373
KEYWORDS
SOURCE
synthetic construct.
synthetic construct.
artificial sequences.
1 (bases 1 to 30)
REFERENCE
Benoit,P., Deneffe,P., Pericaudet,M., Seguret,S. and Vigne,E.
RECOMBINANT VIRUSES AND THEIR USE IN GENE THERAPY
EUREC: W5 942507-A 9 10 NOV-1994;
RHONE POULENC RORER SA (FR)
Other publication AU 6572294 941121
Other publication ZA 9402980 950119
Other publication CA 2161679 941119
Other publication FI 950154 951027
Other publication NO 944924 951026
Other publication FR 2704556 941104
Other publication BR 9406669 960130.
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A4031959.1  GI:5946248
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unknown.
REFERENCE
Unclassified.
1 (bases 1 to 30)
Benoit,P., Deneffe,P., Pericaudet,M., Seguret,S. and Vigne,E.
Recombinant -HepB- viruses consisting an inserted gene encoding
apolipoprotein and their use in gene therapy for
cystic fibrosis
Patent: US 5866551-A 9 02-SEP-1999;
Location/Qualifiers
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/organism="unknown"
JOURNAL
FEATURES
SOURCE

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BASE COUNT      11 a      8 c      10 g      1 t
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Query Match
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Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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|||||
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Search completed: July 21, 2003, 14:35:00
Job time : 322.497 secs

Best Local Similarity 60.28; Score 13; DB 6; Length 24;
 Query Match 43.38; Score 13; DB 6; Length 24;
 Best Local Similarity 76.28; Pred. No. 11e+06;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

LOCUS A46203
 DEFINITION Sequence 19 from Patent WO9208170.
 ACCESSION A46203
 VERSION A46203.1 GI:330451
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE 1 (bases 1 to 32)
 AUTHORS Knight, S.J., Davies, K.E., Hirst, M.C. and Flannery, A.V.
 TITLE METHOD FOR DETECTION OF THE FRASILE X STRIKE
 JOURNAL MEDICAL RES. COUNCIL (GB)
 COMMENT Other Publication AU 6803094 941220.
 FEATURES
 source location/Qualifiers
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BASE COUNT 4 a 5 c 12 g 11 t
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 Query Match 44.14; Score 13; DB 6; Length 32;
 Best Local Similarity 60.28; Pred. No. 8.5e+05;
 Matches 18; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

LOCUS A46203
 DEFINITION Sequence 10 from Patent WO9208170.
 ACCESSION A46203
 VERSION A46203.1 GI:330451
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Makoff, A.J.
 TITLE HUMAN GUT FLORA
 JOURNAL HUMAN GUT FLORA
 COMMENT Patent: WO 952609-A 10-24-AUG-1995;
 WELLCOME FOUND (GB)
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 ORGANISM
 SOURCE
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Makoff, A.J.
 TITLE HUMAN GUT FLORA
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 COMMENT Patent: WO 952609-A 10-24-AUG-1995;
 WELLCOME FOUND (GB)
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BASE COUNT 6 a 2 c 11 g 4 t
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 DEFINITION Sequence 444 from Patent WO921992.
 ACCESSION AX196737
 VERSION AX196737.1 GI:15198493
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE 1 (bases 1 to 25)
 AUTHORS Hauge, B.M., Wang, M.L., Parsons, J.D. and Paterson, J.H.
 TITLE Nucleic acid molecules and their use in the detection of
 cyst nematode resistance
 JOURNAL PATENT: WO 915637-A 444 19-09-2001;
 MONSANTO COMPANY (US)
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 ACCESSION A46203
 VERSION A46203.1 GI:330451
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Makoff, A.J.
 TITLE HUMAN GUT FLORA
 JOURNAL HUMAN GUT FLORA
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 WELLCOME FOUND (GB)
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 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

LOCUS A46203
 DEFINITION Sequence 10 from Patent WO9208170.
 ACCESSION A46203
 VERSION A46203.1 GI:330451
 KEYWORDS
 ORGANISM
 SOURCE
 REFERENCE 1 (bases 1 to 24)
 AUTHORS Makoff, A.J.
 TITLE HUMAN GUT FLORA
 JOURNAL HUMAN GUT FLORA
 COMMENT Patent: WO 952609-A 10-24-AUG-1995;
 WELLCOME FOUND (GB)
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 source location/Qualifiers
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BASE COUNT 6 a 2 c 11 g 4 t
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SOURCE          HUMAN
ORGANISM        Homo sapiens
REFERENCE       1
AUTHORS        Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
TITLE          Obesity associated qualitative marker maps
JOURNAL        GENSER (FR)
PATENT: WO 0206525-A 253 24 JAN-2002;
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Best Local Similarity 43.3%, Prod No 9.9e+05;
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DB             18 CAGAGACAGCAGACAGAGA 1
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DEFINITION     Sequence 25 from Patent US 670790
ACCESSION      AR204662
VERSION        AR204662.1
KEYWORDS       Unclassified.
SOURCE        Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 24)
AUTHORS       Elling Model,F.A., Oster,M., Collipier,T., Friedman,F.M.,
              Hyden,M., Ylasek,M.F., Roberts,F.H., Jr., Fiedler,C., and
              Strong,S.D.
TITLE         Reagents and methods useful for detecting diseases of the
              gastrointestinal tract
JOURNAL       Patent: US 670790-A 25 09-APR-2002;
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Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY             11 ACCAATGATGATGATGAT 20
DB             18 ATTCATGATGATGATGAT 1
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LOCUS          AX104181
DEFINITION     Sequence 15 from Patent WO 020796
ACCESSION      AX104181
VERSION        AX104181.1
KEYWORDS       Synthetic construct,
              artificial sequences.
SOURCE        Synthetic construct,
              artificial sequences.
ORGANISM       Synthetic construct,
              artificial sequences.
REFERENCE      1 (bases 1 to 26)
AUTHORS       Kries,A.M., Schetter,C., and Vollmer,D.C.
TITLE         Immunostimulatory nucleic acids
JOURNAL        Patent: WO 0122972-A 373 05-APR-2001;

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FEATURES
  SOURCE        Location/Qualifiers
               /db_xref="taxon:9606"
               /organism="synthetic construct"
               /db_xref="taxon:9606"
BASE COUNT     2 a 4 c 4 g 10 t
ORIGIN
Query Match    44.0%, Score 13.2, DB 6; Length 26;
Best Local Similarity 43.3%, Prod No 8.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY             23 GACACAGACAGACACAC 6
DB             23 GACACAGACAGACACAC 6
RESULT 24
LOCUS          AX356687
DEFINITION     Sequence 715 from Patent WO0207843.
ACCESSION      AX356687
VERSION        AX356687.1
KEYWORDS       Synthetic construct,
              artificial sequences.
SOURCE        Synthetic construct,
              artificial sequences.
ORGANISM       Synthetic construct,
              artificial sequences.
REFERENCE      1
AUTHORS       Wehrli,J. and Hartmann,U.
TITLE         Methode for enhancing antibody induced cell lysis and treating
              cancer
JOURNAL        Patent: WO 0107947-A 71 07-11-01;
              UNIVERSITY OF IOWA RESEARCH FOUNDATION (US)
FEATURES
  SOURCE        Location/Qualifiers
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               /db_xref="taxon:9606"
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               /db_xref="taxon:9606"
BASE COUNT     0 a 4 c 10 g 12 t
ORIGIN
Query Match    44.0%, Score 13.2, DB 6; Length 26;
Best Local Similarity 43.3%, Prod No 8.7e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
CY             23 GACACAGACAGACACAC 6
DB             23 GACACAGACAGACACAC 6
RESULT 25
LOCUS          179309
DEFINITION     Sequence 12 from Patent US 570796.
ACCESSION      179309
VERSION        179309.1
KEYWORDS       Unknown.
SOURCE        Unknown.
ORGANISM       Unknown.
REFERENCE      1 (bases 1 to 30)
AUTHORS       Gellat,J. and Beutel,B.
TITLE         Method for selecting nucleic acids on the basis of structure
JOURNAL        Patent: US 570796-A 12 13 JAN-1998;
FEATURES
  SOURCE        Location/Qualifiers
               /db_xref="taxon:9606"
               /organism="unknown"
BASE COUNT     2 a 4 c 6 g 18 t
ORIGIN
Query Match    41.0%, Score 13.2, DB 6; Length 33;

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RESULT 17
 LOCUS A12182 10 bp DNA linear PAT 08-JUL-1996
 DEFINITION *Escherichia coli* receptor for phage.
 ACCESSION AF1821
 VERSION AF1821 GI:167375
 KEYWORDS
 SOURCE synthetic construct
 ORGANISM *Escherichia coli*
 FEATURES
 source
 1..30
 /organism="synthetic construct"
 /db_xref="taxon:46240"
 BASE COUNT 12 a 10 c 1 g 5 t
 ORIGIN

Query Match 45.3% Score 13.4; DB 6; Length 30;
 Best Local Similarity 80.0%; Pred. No. 5.9e+05;
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

2Y 5 AGACAGCCTAAATATATATAT 24
 ||||| ||||| ||||| |||||
 10 AATGACATATAAACAATAC 25

RESULT 18
 LOCUS AX487848/c 23 bp DNA linear PAT 16-AUG-2002
 DEFINITION *Escherichia coli* from Patient M00183767.
 ACCESSION AX487848
 VERSION AX487848 GI:22319248
 KEYWORDS
 SOURCE *Candida albicans*
 ORGANISM *Candida albicans*
 FEATURES
 source
 1..23
 /organism="Candida albicans"
 /db_xref="taxon:4976"
 BASE COUNT 3 a 5 c 6 g 9 t
 ORIGIN

Query Match 44.7% Score 13.4; DB 6; Length 23;
 Best Local Similarity 73.9%; Pred. No. 7.1e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2Y 4 AAGAGATACCAAGATCAACCA 26
 ||||| ||||| ||||| |||||
 23 AAGATGACCAAGAGGCTTACCA 1

RESULT 19
 LOCUS AX156335/c 24 bp DNA linear PAT 06-FEB-2002
 DEFINITION *Escherichia coli* from Patient M00183767.
 ACCESSION AX156335
 VERSION AX156335 GI:18620840
 KEYWORDS
 SOURCE *Escherichia coli*
 ORGANISM *Escherichia coli*
 FEATURES
 source
 1..24
 /organism="Escherichia coli"
 /db_xref="taxon:46240"
 BASE COUNT 0 a 1 c 13 g 10 t
 ORIGIN

Query Match 44.7% Score 13.4; DB 6; Length 24;
 Best Local Similarity 73.9%; Pred. No. 7.1e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

TITLE Crystallization of 4 diphosphopyridine 2,6-diphosphopyridine synthase
 JOURNAL Patent WO 019769-A 8 NOV 2001
 THE SALK INSTITUTE BIOENGINEERING INDUSTRIAL ASSOCIATION INC. 01
 LOCATION/Qualifiers
 1..24
 /organism="Escherichia coli"
 /db_xref="taxon:46240"
 /note="GFP ME synthase antisense oligo"

BASE COUNT 0 a 1 c 13 g 10 t
 ORIGIN

Query Match 44.7% Score 13.4; DB 6; Length 24;
 Best Local Similarity 73.9%; Pred. No. 7.3e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2Y 5 AGACAGCCTAAATATATATAT 29
 ||||| ||||| ||||| |||||
 24 AAGATGACCAAGAGGCTTACCA 2

RESULT 20
 LOCUS E36189 29 bp DNA linear PAT 01-JAN-2001
 DEFINITION *Escherichia coli* from Patient M00183767.
 ACCESSION E36189
 VERSION E36189 GI:18626416
 KEYWORDS
 SOURCE *Escherichia coli*
 ORGANISM *Escherichia coli*
 FEATURES
 source
 1..29
 /organism="Escherichia coli"
 /db_xref="taxon:46240"
 BASE COUNT 4 a 4 c 8 g 13 t
 ORIGIN

Query Match 44.7% Score 13.4; DB 6; Length 29;
 Best Local Similarity 73.9%; Pred. No. 7.1e+05;
 Matches 17; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

2Y 4 AAGAGATACCAAGATCAACCA 26
 ||||| ||||| ||||| |||||
 24 AAGATGACCAAGAGGCTTACCA 2

RESULT 21
 LOCUS AX378464/c 19 bp DNA linear PAT 10-MAR-2002
 DEFINITION *Escherichia coli* from Patient M00183767.
 ACCESSION AX378464
 VERSION AX378464 GI:19574317
 KEYWORDS
 SOURCE *Escherichia coli*
 ORGANISM *Escherichia coli*
 FEATURES
 source
 1..19
 /organism="Escherichia coli"
 /db_xref="taxon:46240"
 BASE COUNT 4 a 4 c 8 g 13 t
 ORIGIN

AUTHORS Northern, L.T., Claiborne, R., Greenwald, L., Lindquist, P.H. and Saksela, E.
 TITLE Genetic polymorphism and polymorphic patterns for assessing disease status, and compositions for use thereof
 JOURNAL Patent, WO 00/040704 A1, 2000, 2000-01-20
 FEATURES
 LOCATION/Qualifiers
 1. 20
 /organism="synthetic construct"
 /db_xref="taxon:12101"
 /note="oligonucleotide primer"
 BASE COUNT 1 a 6 c 5 g 8 t
 ORIGIN
 Query Match 46.0% Score 13.6; E=6; Length 20
 Best Local Similarity 89.0% From No. 4 (1993)
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0

CY 4 AGAGACACCAAGACA 20
 DB 19 AAGATGATGACAGACA 1

RESULT 13
 AX037441/c
 LOCUS Sequence 26 bp. From Northern, L.T.
 DEFINITION AX037441
 ACCESSION AX037441
 VERSION AX037441 GI:11226667
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS Northern, L.T., Claiborne, R., Greenwald, L., Lindquist, P.H. and Saksela, E.
 TITLE Genetic polymorphism and polymorphic patterns for assessing disease status, and compositions for use thereof
 JOURNAL Patent, WO 00/040704 A1, 2000, 2000-01-20
 FEATURES
 LOCATION/Qualifiers
 1. 20
 /organism="synthetic construct"
 /db_xref="taxon:12101"
 /note="oligonucleotide primer"
 BASE COUNT 1 a 6 c 5 g 8 t
 ORIGIN
 Query Match 46.0% Score 13.6; E=6; Length 20
 Best Local Similarity 89.0% From No. 4 (1993)
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0

CY 4 AGAGACACCAAGACA 20
 DB 19 AAGATGATGACAGACA 1

RESULT 14
 AX118063
 LOCUS Sequence 24 bp. From Northern, L.T.
 DEFINITION AX118063
 ACCESSION AX118063
 VERSION AX118063 GI:11835011
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS Northern, L.T., Claiborne, R., Greenwald, L., Lindquist, P.H. and Saksela, E.

TITLE Genetic polymorphism and polymorphic patterns for assessing disease status, and compositions for use thereof
 JOURNAL Patent, WO 00/040704 A1, 2000, 2000-01-20
 FEATURES
 LOCATION/Qualifiers
 1. 24
 /organism="synthetic construct"
 /db_xref="taxon:12101"
 /note="primer"
 BASE COUNT 9 a 6 c 5 g 7 t
 ORIGIN
 Query Match 46.0% Score 13.6; E=6; Length 24
 Best Local Similarity 89.0% From No. 5e+05
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0

CY 4 GAGACCAAGACACAC 24
 DB 4 GAGACCAAGACACAC 20

RESULT 15
 AR177327
 LOCUS Sequence 29 bp. From Patent US 5,012,322.
 DEFINITION AR177327
 ACCESSION AR177327
 VERSION AR177327.1 GI:17919682
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS Edwards, J., Buchanan, M., Dwyer, A., and Bougeny, J.
 TITLE Complementary DNAs
 JOURNAL Patent, US 5,012,322, 1991, 1991-01-01
 FEATURES
 LOCATION/Qualifiers
 1. 29
 /organism="unknown"
 BASE COUNT 10 a 8 c 9 g 2 t
 ORIGIN
 Query Match 46.0% Score 13.6; E=6; Length 29
 Best Local Similarity 89.0% From No. 5e+05
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0

CY 5 AGAGACACCAAGACAC 24
 DB 6 AGAGACACCAAGACAC 25

RESULT 16
 A26587
 LOCUS Sequence 30 bp. From Northern, L.T.
 DEFINITION A26587
 ACCESSION A26587
 VERSION A26587 GI:118251
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS Northern, L.T., Claiborne, R., Greenwald, L., Lindquist, P.H. and Saksela, E.

TITLE Genetic polymorphism and polymorphic patterns for assessing disease status, and compositions for use thereof
 JOURNAL Patent, WO 00/040704 A1, 2000, 2000-01-20
 FEATURES
 LOCATION/Qualifiers
 1. 30
 /organism="synthetic construct"
 /db_xref="taxon:12101"
 /note="primer"
 BASE COUNT 12 a 10 c 3 g 5 t
 ORIGIN
 Query Match 45.3% Score 13.6; E=6; Length 30
 Best Local Similarity 89.0% From No. 5e+05
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0

CY 5 AGAGACACCAAGACAC 24
 DB 10 AGAGACACCAAGACAC 29

FEATURES Location/Qualifiers
 source 1..22
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="5' 3'-nucleotide primer"
 ORIGIN
 BASE COUNT a 8 7 2 g 5 t
 Query Match 50.7% Score 11.21 E 6 Length 20
 Best local similarity 55.0% Ident No. 1 gaps 0
 Matches 17 Conservative 0 Mismatches 3 Indels 0 Gaps 0

Query 10 CACCAAGACACTACCAACA 29
 Db 3 CACCAATACACTACTTTCACA 22

RESULT 4
 AB2168/c
 LOCUS
 DEFINITION Sequence 3 from Patent WO9856928.
 ACCESSION AB2168
 VERSION A0109.1 GI:172293
 KEYWORDS
 SOURCE unidentified.
 ORGANISM unidentified.
 REFERENCE 1 (bases 1 to 26)
 AUTHORS Harrison M.M. and De G.F.
 TITLE INCREASED FREQUENCY OF REPEATING AT NUCS POLYMERASE LINE PATENT
 JOURNAL PATENT: WO 9856928-A 3 17-DEC-1998
 HARRISON MICHAEL MARIE (ND), GEUS BERNARD DE (ND)
 Location/Qualifiers
 1..26
 /organism="unidentified"
 /db_xref="taxon:32644"
 ORIGIN
 BASE COUNT 0 a 1 c 11 g 14 t

Query Match 50.7% Score 11.21 E 6 Length 20
 Best local similarity 55.0% Ident No. 1 gaps 0
 Matches 17 Conservative 0 Mismatches 3 Indels 0 Gaps 0

Query 7 AACACCAAGACACTACCAACA 26
 Db 20 AACACCAAGACACTACCAACA 1

RESULT 5
 AR166095/c
 LOCUS
 DEFINITION Sequence 13 from patent US 6282949.
 ACCESSION AR166095
 VERSION AR166095.1 GI:16641267
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 19)
 AUTHORS Horiuchi F.M.
 TITLE Multiple cloning vector application
 JOURNAL Patent: US 6282949-A 1 15 NOV 2001
 Location/Qualifiers
 1..19
 /organism="Unknown"
 ORIGIN
 BASE COUNT 3 a 3 2 c 4 g 9 t

Query Match 48.8% Score 14.41 E 6 Length 19
 Best local similarity 53.9% Ident No. 2 gaps 0
 Matches 17 Conservative 0 Mismatches 1 Indels 0 Gaps 0

Query 8 GACCAAGACACTA 23

Db 16 GACCAAGACACTA 3

RESULT 6
 AX444384/c
 LOCUS
 DEFINITION Sequence 839 from Patent WO9756649.
 ACCESSION AX444384
 VERSION AX444384.1 JI:276362
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Gunderson K.
 TITLE Probes and decoder oligonucleotides
 JOURNAL Patent: WO 9216649-A 849 24-SEP-2002
 Illumina, Inc. (US)
 Location/Qualifiers
 1..24
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 /note="Computer Generated Probe Sequence."
 ORIGIN
 BASE COUNT 2 a 6 c 7 g 9 t

Query Match 48.8% Score 14.41 E 6 Length 23
 Best local similarity 53.9% Ident No. 2 gaps 0
 Matches 15 Conservative 0 Mismatches 5 Indels 0 Gaps 0

Query 24 AACCCGAAAGACACTACACTAT 1
 Db 24 AACCCGAAAGACACTACACTAT 1

RESULT 7
 AB068871/c
 LOCUS
 DEFINITION Synthetic construct DNA, reverse primer for human STS STS PAFRFR at 1p36.
 ACCESSION AB068871
 VERSION AB068871.1 GI:15129675
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM synthetic construct.
 REFERENCE 1
 AUTHORS Chen, H.C., Hayashi, Y., Wang, S., Takada, E., Mochizuki, H., Maruyama, N., Inayama, J., Hosoda, F., Akai, Y., Mizushima, H., Matsushita, A., Matsui, M., Takajima, A., Iwano, H., Horiuchi, F. and Soda, E.
 TITLE A BAC-cloned STS-containing map spanning a 35-Mb region of human chromosome 1p35-p36
 JOURNAL Chromosomes 74 (1), 55-70 (2001)
 MEDLINE 2120192
 REFERENCE 2 (bases 1 to 20)
 AUTHORS Horiuchi, F.
 TITLE Direct Submission
 JOURNAL Submitted (04 NOV 2001) Akira Horiuchi, Graduate University School of Medicine, Kawasaki University of Medical Welfare, 1030 Shogino-cho, Asahi-ku, Sendai, Miyagi 980-8557, Japan. E-mail: horiuchi@med.kawasaki-u.ac.jp. Tel:81 22 717 8042, Fax:81-22-717-8047
 Location/Qualifiers
 1..20
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 ORIGIN
 BASE COUNT 1 a 2 c 9 g 9 t

misc_feature
 1..20
 /note="reverse primer for human STS STS PAFRFR at 1p36
 was reverse obtained from Clontech Lab. / db_xref="taxon:32630"
 /note="AF01-11"
 ORIGIN
 BASE COUNT 1 a 2 c 9 g 9 t

•
•

Query Match 42.7% Score 12.8; DB 10; Length 34;
 Best Local Similarity 70.8%; Prod. No. 3e+05; 7; Indels 0; Gaps 0;
 Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 6 TTGGGACGAGAGATTGTTTCTGT 29
 DB 1 TTGGGACGAGAGGTTTCTTTT 24

RESULT 40
 AV958709

LOCUS 34 bp mRNA linear EST 14-MAR-2002
 DEFINITION AV958709 Noli Satoh unpublished cDNA library, young adult Ciona

intestinalis cDNA clone cladi0124 5', mRNA sequence.

AV958709

AV958709.1 GI:19447008

KEYWORDS

SOURCE

ORGANISM

EST.
 Ciona intestinalis.

Ciona intestinalis

Phlebobranchia: Clonidae; Ciona.

1 (bases 1 to 34)

Satoh, N., Satoh, Y., Kohara, Y. and Shin-I, T.

Expressed genes in Ciona intestinalis

Unpublished (2000)

Contact: Noli Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satchiasaidian.2001@yoda.uw.ac.jp.

Location/Qualifiers

1 .34

/organism="Ciona intestinalis"

/db_xref="taxon:7719"

/clone="cladi0124"

/note="17 70.8% 1 of 11803 cDNA library, young

adult"

/tissue_type="whole animal"

/dev_stage="young adult"

/note="Vector, plasmid SK"

BASE COUNT 2 a 7 c 6 g 19 t

ORIGIN

Query Match 42.7% Score 12.8; DB 10; Length 34;

Best Local Similarity 70.8%; Prod. No. 3e+05; 7; Indels 0; Gaps 0;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

CY 6 TTGGGACGAGAGATTGTTTCTGT 29

DB 1 TTGGGACGAGAGGTTTCTTTT 24

Search completed: July 21, 2003, 15:46:59

Job time : 790.76 secs

FEATURES
Source

1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
/issue_type="whole animal"
/dev_stage="young adult"
/dev_stage="young adult"
/dev_stage="young adult"

BASE COUNT
ORIGIN

Query Match: 42.7%, Score 12.8, DB 10, Length 34,
Best Local Similarity 70.8%, Pred. No. 3e+05,
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

2Y
db 1 TTTGGCAAGAGGATTTCTCT 29
1 TTTGGCAAGAGGATTTCTCT 24

RESULT 37
LOCUS AV953949 34 bp mRNA linear EST 14 MAR 2002
DEFINITION AV953949 Homo Sapiens cDNA library, young adult Clona
intestinalis cDNA clone clon90918 5', mRNA sequence.
ACCESSION AV953949 1 GI:19442248
VERSION EST
KEYWORDS Clona intestinalis.
SOURCE Clona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Actinoptera; Percomorphi;
Phlebotominae; Clonidae; Clona.
REFERENCE 1 (bases 1 to 34)
AUTHOR Satoh,N., Satoh,Y., Kobata,Y. and Shin,I.T.
TITLE Expressed genes in Clona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@zoology.kyoto-u.ac.jp

FEATURES
Source

1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
/issue_type="whole animal"
/dev_stage="young adult"
/dev_stage="young adult"
/dev_stage="young adult"

BASE COUNT
ORIGIN

Query Match: 42.7%, Score 12.8, DB 10, Length 34,
Best Local Similarity 70.8%, Pred. No. 3e+05,
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

2Y
db 1 TTTGGCAAGAGGATTTCTCT 29
1 TTTGGCAAGAGGATTTCTCT 24

RESULT 38
LOCUS AV957202 34 bp mRNA linear EST 14 MAR 2002
DEFINITION AV957202 Homo Sapiens cDNA library, young adult Clona
intestinalis cDNA clone clon90919 5', mRNA sequence.

ACCESSION
VERSION AV957202 1 GI:19444401
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Actinoptera; Percomorphi;
Phlebotominae; Clonidae; Clona.
REFERENCE 1 (bases 1 to 34)
AUTHOR Satoh,N., Satoh,Y., Kobata,Y. and Shin,I.T.
TITLE Expressed genes in Clona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@zoology.kyoto-u.ac.jp

FEATURES
Source

1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
/issue_type="whole animal"
/dev_stage="young adult"
/dev_stage="young adult"

BASE COUNT
ORIGIN

Query Match: 42.7%, Score 12.8, DB 10, Length 34,
Best Local Similarity 70.8%, Pred. No. 3e+05,
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0;

2Y
db 1 TTTGGCAAGAGGATTTCTCT 29
1 TTTGGCAAGAGGATTTCTCT 24

RESULT 39
LOCUS AV958100 34 bp mRNA linear EST 14 MAR 2002
DEFINITION AV958100 Homo Sapiens cDNA library, young adult Clona
intestinalis cDNA clone clon90918 5', mRNA sequence.
ACCESSION AV958100 1 GI:19446199
VERSION EST.
KEYWORDS Clona intestinalis.
SOURCE Clona intestinalis.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Actinoptera; Percomorphi;
Phlebotominae; Clonidae; Clona.
REFERENCE 1 (bases 1 to 34)
AUTHOR Satoh,N., Satoh,Y., Kobata,Y. and Shin,I.T.
TITLE Expressed genes in Clona intestinalis
JOURNAL Unpublished (2000)
COMMENT Contact: Nori Satoh
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606 8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@zoology.kyoto-u.ac.jp

FEATURES
Source

1. 34
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Nori Satoh unpublished cDNA library, young adult"
/issue_type="whole animal"
/dev_stage="young adult"
/dev_stage="young adult"

BASE COUNT
ORIGIN

REFERENCE
1 (bases 1 to 34)
AUTHORS
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Saitoh
Department of Zoology
Kyoto University
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Email: saito@zoology.kyoto-u.ac.jp

FEATURES
Source
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Nori Saitoh unpublished cDNA library, young adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBlueScript SK"

BASE COUNT
a 4 c 3 g 3 t 17

ORIGIN
Query Match 42.7%, E-value 12.5, E-110, Length 34,
Best local similarity 70.6%, Field No. 3605,
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY
1 TCGGCAAGAGGATGTTTCTTCT 29
1 TCGGCAAGAGGATGTTTCTTCT 24

RESULT 34
AV9538797
LOCUS
AV9538797 Nori Saitoh unpublished cDNA library, young adult cDNA
intestinalis cDNA clone cl089824 29, cDNA sequence.
VERSION
AV9538797
KEYWORDS
EST.
EST: 19442096
SOURCE
Ciona intestinalis.
Ciona intestinalis.
Eukaryota, Metazoa, Chordata, Vertebrata, Ascidiacea, Enteromorpha,
Phlebobranchia, Clonidae, Ciona.
1 (bases 1 to 34)
AUTHORS
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Saitoh
Department of Zoology
Kyoto University
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Email: saito@zoology.kyoto-u.ac.jp

FEATURES
Source
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Nori Saitoh unpublished cDNA library, young adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBlueScript SK"

BASE COUNT
a 3 c 3 g 3 t 17

ORIGIN
Query Match 42.7%, E-value 12.5, E-110, Length 34,
Best local similarity 70.6%, Field No. 3605,
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY
1 TCGGCAAGAGGATGTTTCTTCT 29
1 TCGGCAAGAGGATGTTTCTTCT 24

QY
6 TCGGCAAGAGGATGTTTCTTCT 29
1 TCGGCAAGAGGATGTTTCTTCT 24

RESULT 35
AV9538843
LOCUS
AV9538843 Nori Saitoh unpublished cDNA library, young adult cDNA
intestinalis cDNA clone cl089824 29, cDNA sequence.
VERSION
AV9538843
KEYWORDS
EST.
EST: 31194412
SOURCE
Ciona intestinalis.
Ciona intestinalis.
Eukaryota, Metazoa, Chordata, Vertebrata, Ascidiacea, Enteromorpha,
Phlebobranchia, Clonidae, Ciona.
1 (bases 1 to 34)
AUTHORS
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Saitoh
Department of Zoology
Kyoto University
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Email: saito@zoology.kyoto-u.ac.jp

FEATURES
Source
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Nori Saitoh unpublished cDNA library, young adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBlueScript SK"

BASE COUNT
a 2 c 3 g 3 t 19

ORIGIN
Query Match 42.7%, E-value 12.5, E-110, Length 34,
Best local similarity 70.6%, Field No. 3605,
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY
1 TCGGCAAGAGGATGTTTCTTCT 29
1 TCGGCAAGAGGATGTTTCTTCT 24

RESULT 36
AV9538906
LOCUS
AV9538906 Nori Saitoh unpublished cDNA library, young adult cDNA
intestinalis cDNA clone cl089824 29, cDNA sequence.
VERSION
AV9538906
KEYWORDS
EST.
EST: 31194415
SOURCE
Ciona intestinalis.
Ciona intestinalis.
Eukaryota, Metazoa, Chordata, Vertebrata, Ascidiacea, Enteromorpha,
Phlebobranchia, Clonidae, Ciona.
1 (bases 1 to 34)
AUTHORS
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
TITLE
Expressed genes in *Ciona intestinalis*
JOURNAL
Unpublished (2000)
COMMENT
Contact: Nori Saitoh
Department of Zoology
Kyoto University
Saitoh, N., Saitoh, Y., Kohara, Y. and Shin-i, T.
Tel: 81-75-753-4081
Fax: 81-75-753-4081
Email: saito@zoology.kyoto-u.ac.jp

FEATURES
Source
1..34
/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone_lib="Nori Saitoh unpublished cDNA library, young adult"
/tissue_type="whole animal"
/dev_stage="young adult"
/note="Vector: pBlueScript SK"

BASE COUNT
a 2 c 3 g 3 t 19

ORIGIN
Query Match 42.7%, E-value 12.5, E-110, Length 34,
Best local similarity 70.6%, Field No. 3605,
Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY
1 TCGGCAAGAGGATGTTTCTTCT 29
1 TCGGCAAGAGGATGTTTCTTCT 24

[illegible][illegible]

Query Match 42.7% Score 12.8; DB 10; Length 32;

Best Local Similarity 70.8%; Pred. No. 3e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0

CV 6 TGGGACGAGAGGATGTTCTGT 29
|||||
2 TGGGACGAGAGGATGTTCTTTT 25

RESULT 18
AV674389

LOCUS AV674389 32 bp mRNA linear EST 06-OCT-2000
DEFINITION cDNA clone c1b15q22.5, mRNA sequence.

ACCESSION AV674389.1 GI:10113388
VERSION AV674389.1
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis.

REFERENCE Eubrychta, Metarza, Chertkov, Chertkov, Aschileva, Erdemoglu,
Phlebotrichia; Clonidae; Clona.
1 (bases 1 to 32)
Sato, N., Sato, Y., Kohara, Y. and Shin-I, T.
Expressed genes in Clona intestinalis
Unpublished (2000)

TITLE
JOURNAL
COMMENT
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sakobase@kcl.kyoto-u.ac.jp

FEATURES
Source
1..32
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="c1b15q22"
/tissue_type="whole animal"
/dev_stage="tailbud"
/vector="pBluescript SK"

BASE COUNT 3 a 3 c 7 g 19 t

Query Match 42.7% Score 12.8; DB 10; Length 32;

Best Local Similarity 70.8%; Pred. No. 3e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0

CV 6 TGGGACGAGAGGATGTTCTGT 29
|||||
2 TGGGACGAGAGGATGTTCTTTT 25

RESULT 19
AV675687

LOCUS AV675687 32 bp mRNA linear EST 05-OCT-2000
DEFINITION cDNA clone c1b15q25.5, mRNA sequence.

ACCESSION AV675687.1 GI:10113686
VERSION AV675687.1
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis.

REFERENCE Eubrychta, Metarza, Chertkov, Chertkov, Aschileva, Erdemoglu,
Phlebotrichia; Clonidae; Clona.
1 (bases 1 to 32)
Sato, N., Sato, Y., Kohara, Y. and Shin-I, T.
Expressed genes in Clona intestinalis
Unpublished (2000)

TITLE
JOURNAL
COMMENT
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sakobase@kcl.kyoto-u.ac.jp

Query Match 42.7% Score 12.8; DB 10; Length 32;

Best Local Similarity 70.8%; Pred. No. 3e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0

CV 6 TGGGACGAGAGGATGTTCTGT 29
|||||
2 TGGGACGAGAGGATGTTCTTTT 25

RESULT 20
AV948018

LOCUS AV948018 32 bp mRNA linear EST 14-MAR-2001
DEFINITION cDNA clone c1b15q22.5, mRNA sequence.

ACCESSION AV948018.1 GI:19425777
VERSION AV948018.1
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis.

REFERENCE Eubrychta, Metarza, Chertkov, Chertkov, Aschileva, Erdemoglu,
Phlebotrichia; Clonidae; Clona.
1 (bases 1 to 32)
Sato, N., Sato, Y., Kohara, Y. and Shin-I, T.
Expressed genes in Clona intestinalis
Unpublished (2000)

TITLE
JOURNAL
COMMENT
Department of Zoology
Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: sakobase@kcl.kyoto-u.ac.jp

FEATURES
Source
1..32
/organism="Clona intestinalis"
/db_xref="taxon:7719"
/clone="c1b15q22"
/tissue_type="whole animal"
/dev_stage="young adult"
/vector="pBluescript SK"

BASE COUNT 2 a 3 c 7 g 19 t

Query Match 42.7% Score 12.8; DB 10; Length 32;

Best Local Similarity 70.8%; Pred. No. 3e+05;

Matches 17; Conservative 0; Mismatches 7; Indels 0; Gaps 0

CV 6 TGGGACGAGAGGATGTTCTGT 29
|||||
2 TGGGACGAGAGGATGTTCTTTT 25

RESULT 21
AV965254

LOCUS AV965254 32 bp mRNA linear EST 21-MAR-2001
DEFINITION cDNA clone c1b15q22.5, mRNA sequence.

ACCESSION AV965254.1 GI:10113686
VERSION AV965254.1
KEYWORDS EST.
SOURCE Clona intestinalis.
ORGANISM Clona intestinalis.

REFERENCE Eubrychta, Metarza, Chertkov, Chertkov, Aschileva, Erdemoglu,
Phlebotrichia; Clonidae; Clona.
1 (bases 1 to 32)
Sato, N., Sato, Y., Kohara, Y. and Shin-I, T.
Expressed genes in Clona intestinalis
Unpublished (2000)

Method 19, Conservative 0, Mismatch 9, Indels 0, Gaps 0

Query Match 42.74, Score 12.8, DB 17, Length 29;
Best Local Similarity 70.88; Pred. No. 3e+05;

RESULT 12
Accession AV675044 29 bp, RNA, linear, 280 bp, FEB 2001
Definition 280 bp cDNA, Mus musculus muscle tissue library Mus musculus genomic
Accession AV675044 1 611005952
Version AV675044.1 611005952
Keywords house mouse
Source Mus musculus
Organism Mus musculus
Reference Eukaryotic, Mus musculus, Chondrichthyes, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Authors I. Bases 1 to 29
Title 280 bp cDNA, Mus musculus muscle tissue library Mus musculus genomic
Comment Mus musculus muscle tissue library Mus musculus genomic
Title 280 bp cDNA, Mus musculus muscle tissue library Mus musculus genomic
Comment Mus musculus muscle tissue library Mus musculus genomic

FEATURES
Source location/Qualifiers
1..29
/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="U06200130011"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
/note="Vector: pMD20my. Purified genomic DNA from M. musculus cDNA/cr. (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/theses/) The RNA was hybridized to a cDNA library prepared by repeated passage through a 0.1% polyacrylamide gel. The cDNA was ligated into the blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter-1 RNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD20 (314731114) (pMD20-11). A copy-number inducible derivative of pMD20-11 was prepared. The vector was ligated with adapter complementary to the insert adapters and purified. The sheared, adapter-1 RNA was annealed to the adapter-2 RNA, and transcribed into cDNA. The cDNA was chemically synthesized E. coli XL10-Gold (Stratagene) cells and selected for application to a library."

FASTA COMMENT
ORIGIN
Query Match 42.74, Score 12.8, DB 17, Length 29;
Best Local Similarity 70.88; Pred. No. 3e+05;

Method 17, Conservative 0, Mismatch 9, Indels 0, Gaps 0

Query Match 42.74, Score 12.8, DB 17, Length 29;
Best Local Similarity 70.88; Pred. No. 3e+05;

RESULT 13
Accession AV675087 31 bp, RNA, linear, 280 bp, FEB 2001
Definition 280 bp cDNA, Mus musculus muscle tissue library Mus musculus genomic
Accession AV675087 1 6110113086
Version AV675087.1 6110113086
Keywords house mouse
Source Mus musculus
Organism Mus musculus
Reference Eukaryotic, Mus musculus, Chondrichthyes, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
Authors I. Bases 1 to 31
Title 280 bp cDNA, Mus musculus muscle tissue library Mus musculus genomic
Comment Mus musculus muscle tissue library Mus musculus genomic

FEATURES
Source location/Qualifiers
1..31
/organism="Mus musculus"
/db_xref="taxon:10090"
/db_xref="taxon:10090"
/clone="U06200130011"
/sex="Male"
/lab_host="E. coli strain XL10-Gold, Ti-resistant, F-"
/note="Vector: pMD20my. Purified genomic DNA from M. musculus cDNA/cr. (male) was obtained from the Jackson Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/theses/) The RNA was hybridized to a cDNA library prepared by repeated passage through a 0.1% polyacrylamide gel. The cDNA was ligated into the blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter-1 RNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD20 (314731114) (pMD20-11). A copy-number inducible derivative of pMD20-11 was prepared. The vector was ligated with adapter complementary to the insert adapters and purified. The sheared, adapter-1 RNA was annealed to the adapter-2 RNA, and transcribed into cDNA. The cDNA was chemically synthesized E. coli XL10-Gold (Stratagene) cells and selected for application to a library."

FASTA COMMENT
ORIGIN
Query Match 42.74, Score 12.8, DB 17, Length 29;
Best Local Similarity 70.88; Pred. No. 3e+05;

Query Match 44 84 Score 13.2 DB 13 Length 32

Best Local Similarity 60.28 Pctd Nov 2, 1995

Matches 18 Conservative 9 Mismatches 9 Indels 0 Gaps 0

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

Query Match 44 84 Score 13.2 DB 13 Length 32

BASE COUNT

5 a 3 c 7 g 17 t

ORIGIN

DATE CONT
ORIGIN

```

OY      10 GCAGGAGGAAATTTGTTCTGT 21
          ||| ||| ||| ||| |||
TP      12 GCACAAAGGAGTTGTTTGT 31

```

ABSTRACTION	AW672830
DESCRIPTION	AW672830
KEYWORDS	ESP.
SOURCE	Cioma intestinalis.

Department of Geology
Yamaguchi University
Sakyo-ku, Yamaguchi
Tel: 81-75-753-4081

300

ORIGIN

oy 4 ATTCGGGACGAGCGAATTTTCTTGT 20
| | | | |
7b 2 AATTCGGCAGAGGTTTTTTTTT 27

RESULT 4

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source
1. .31
/organism="Cic
/db_xref="taxo
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	Query Match	4.0%	0
Best Local Similarity	69.28	0	0
Matches	18	Conservative	97

RESULT 5

2000

COMMENT

Email: tschini@genes.mcgill.ca
 FEATURES location/Qualifiers
 source 1. .32

C 956	8.6	28.7	24 17	AC243947	AC243947 IM0327106
C 970	8.6	28.7	24 17	AC277750	AC277750 IM0317893
C 958	8.6	28.7	24 17	AC243437	AC243437 IM0317893
C 959	8.6	28.7	24 17	AC283307	AC283307 IM0116422
C 960	8.6	28.7	24 17	EH951216	EH951216 SALK_0761
C 961	8.6	28.7	24 17	TA124B88P	TA124B88P T. brucei
C 962	8.6	28.7	24 17	TA124B90P	TA124B90P T. brucei
C 963	8.6	28.7	24 17	TA124C37P	TA124C37 T. brucei
C 964	8.6	28.7	24 17	TA156G98P	TA156G98P T. brucei
C 965	8.6	28.7	25 9	AM934937	AM934937 HJ17089.S
C 966	8.6	28.7	25 17	AC233935	AC233935 IM0306112
C 967	8.6	28.7	25 17	AC267893	AC267893 IM0317893
C 968	8.6	28.7	25 17	AC270714	AC270714 IM0317893
C 969	8.6	28.7	25 17	AC271573	AC271573 IM0317893
C 970	8.6	28.7	25 17	AC291064	AC291064 IM0317893
C 971	8.6	28.7	25 17	AC291630P	AC291630P IM0306492
C 972	8.6	28.7	25 17	HM935971	HM935971 SALK_0891
C 973	8.6	28.7	25 17	AM246553	AM246553 D922092.3
C 974	8.6	28.7	26 10	A2736136P	A2736136P IM0309234
C 975	8.6	28.7	26 17	AC247334	AC247334 IM028908P
C 976	8.6	28.7	26 17	AC268239	AC268239 IM0486012
C 977	8.6	28.7	26 17	A2796847	A2796847 IM0333837
C 978	8.6	28.7	26 17	AC278973P	AC278973P IM0332819
C 979	8.6	28.7	26 17	HM116431	HM116431 SALK_0614
C 980	8.6	28.7	26 17	BH860418	BH860418 SALK_0711
C 981	8.6	28.7	27 14	H77242	H77242 YH12310.81
C 982	8.6	28.7	27 17	AC239376	AC239376 IM0309234
C 983	8.6	28.7	27 17	AC250903	AC250903 IM0309234
C 984	8.6	28.7	27 17	BH791823	BH791823 SALK_0614
C 985	8.6	28.7	27 17	TA297F0P	TA297F0P T. brucei
C 986	8.6	28.7	27 17	TA125P72	TA125P72 T. brucei
C 987	8.6	28.7	27 17	TA125P72	TA125P72 T. brucei
C 988	8.6	28.7	28 3	AM66768P	AM66768P TA15637.X
C 989	8.6	28.7	28 14	AM66768P	AM66768P IM0306492
C 990	8.6	28.7	28 17	AC231444	AC231444 IM0317893
C 991	8.6	28.7	28 17	AC234581	AC234581 IM0306492
C 992	8.6	28.7	28 17	AC234581	AC234581 IM0306492
C 993	8.6	28.7	28 17	AC263122	AC263122 IM0486012
C 994	8.6	28.7	28 17	AC263122	AC263122 IM0486012
C 995	8.6	28.7	28 17	AC272641	AC272641 IM0486012
C 996	8.6	28.7	28 17	AC291310P	AC291310P IM0317893
C 997	8.6	28.7	28 17	TA28807P	TA28807P T. brucei
C 998	8.6	28.7	29 17	AM246553	AM246553 EF1732756
C 999	8.6	28.7	29 17	AM246553	AM246553 IM0306492
C1000	8.6	28.7	29 17	AM307336	AM307336 IM0306492

ALIGNMENTS

RESULT 1
 R0064029
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

R0064029 4 bp mRNA linear EST 07 DEC 2001
 R0064029.1 nipa M-111, cultured Xenopus laevis library
 laevis cDNA clone X009827.1, cDNA sequence.
 R0064029
 R0064029.1 nt.1242467
 EST
 African clawed frog.
 ORGANISM
 Xenopus laevis
 Eukaryota; Metazoa; Chordata; Cephalia; Vertebrata; Euteleostomi;
 Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
 Xenopodinae; Xenopus
 (bases 1 to 34)
 Kiyama, A., Toriizawa, Y., Yoshida, Y., Tanabe, T. and Fihara
 Y.
 Referenced from X laevis cod. y
 unpublished (2001)
 Contact: Tadashi Shim-i

1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559 81 6856

FAX: 01 519 81 6835
 Email: shinjo@ncc.nij.go.jp
 Translation/Interpreters
 1. 24
 Source

PAGE 2
ORIGIN

	Query Match	48.3%	Score 12.6	Length 141
Best Local Similarity	66.0% <td>Score 14.4 <td>Length 157 </td></td>	Score 14.4 <td>Length 157 </td>	Length 157	
Matches	29	Mismatches 10	Indels 0	
			gaps 0	

12

5 GGNATTGGGACGAGSTTTTTTTT 33

A2470637

Accession number: AF047063.7 34 bp DNA 1100 bp GSS 04 007 200
 Description: IMC04704.45 Mouse 10 kb P3ase-IH genomic library with infectious genome
 Cloning vector: IMC04704.45 R, DNA sequence.

KEYWORDS

ORGANISMS

REFERENCE

TITLE

JOURNAL
COMMENT

TITLE Mouse whole-genome scaffolding with paired-end reads from 10xT
JOURNAL Plasmid inserts
COMMENT Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Em: 308, Biomedical polymers Research Bldg., 20 N. 2000 E., Ste. 100
84112, USA
Tel: 801.286.5406
Fax: 801.585.7177
Email: dduan@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0284 row: N column: 14
Seq primer: CACACAGGACACGATAGAC
Class: plasmid ends
High quality sequence: 33, 34,
Location/Qualifiers
1..34

High-ability section of sample 34
Location/Qualifiers

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/db xref=taxon:10090"  
/db xref=ncic:m26474"  
/clone_lib=Mouse 10k plasmid library"  
/sex=Male"  
"10090" "m26474" "mouse" "male"  
"10090" "m26474" "mouse" "male"  
musculus C78E/cd (male) was obtained from The Jackson  
Laboratory Maine DNA Resource
```

[illegible]

[illegible]

Publication No. H032035087235A1
GENERAL INFORMATION:
APPLICANT: Daikee, Shanz H.
TITLE OF INVENTION: PROGNOSTIC METHODS FOR BREAST CANCER
FILE REFERENCE: CMC 010/0095
CURRENT APPLICATION NUMBER: HS/09/416,460C
CURRENT FILING DATE: 2001 03 23
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.1
SEQ ID NO 44
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic primer
35 09 816 460C 44

Query Match 44 04: Score 13.2; 79.12; Length 20;
Best local similarity 83.34; Fred. No. 1.9e+04;
Matches 15, Conservative 0, Mismatches 3, Indels 0, Gaps 0;

CY 10 GCAGAGAGAAATTTTCT 27
|||||
DB 20 GCAGAGAGAAATTTCT 3

Search completed: July 21, 2003, 18:30:13
Job time : 83.6397 secs

APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/09/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 66020
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B 66020

Query Match: 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity: 73.5%, Field No: 1,66+04,
 Matches: 17, Conservative: 0, Mismatches: 6, Indels: 0, Gaps: 0

5 TTGGGGAGAGAGAGATTTTGT 27
 24 TCGGGAGAGAGAGCTTTGT 2

RESULT 36
 US-10-098-263B-78475/c
 Sequence 78475, Application US/09/098,263B
 Publication No: US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/10/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 78475
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-78475

Query Match: 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity: 73.5%, Field No: 1,66+04,
 Matches: 17, Conservative: 0, Mismatches: 6, Indels: 0, Gaps: 0

8 GGGAGAGAGATTTTGT 30
 24 GGGAGAGAGATTTTGT 2

RESULT 37
 US-10-098-263B-11071/c
 Sequence 11071, Application US/09/098,263B
 Publication No: US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/09/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 11071
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-11071

Query Match: 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity: 73.5%, Field No: 1,66+04,
 Matches: 17, Conservative: 0, Mismatches: 6, Indels: 0, Gaps: 0

1 GAAATGGAGAGAGATTTGT 23
 23 GAAATGGAGAGAGATTTGT 1

RESULT 38
 US-10-098-263B-11072/c
 Sequence 11072, Application US/09/098,263B
 Publication No: US20030104410A1
 GENERAL INFORMATION:
 APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 3118.1
 CURRENT APPLICATION NUMBER: US/09/098,263B
 CURRENT FILING DATE: 2003-01-08
 PRIOR APPLICATION NUMBER: 60/276,759
 PRIOR FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 131066
 SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
 SEQ ID NO: 11072
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-098-263B-11072

Query Match: 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity: 73.5%, Field No: 1,66+04,
 Matches: 17, Conservative: 0, Mismatches: 6, Indels: 0, Gaps: 0

1 GAAATGGAGAGAGATTTGT 23
 23 GAAATGGAGAGAGATTTGT 1

RESULT 39
 US-10-131-175-10/c
 Sequence 10, Application US/10/131,175
 Publication No: US20030104417A1
 GENERAL INFORMATION:
 APPLICANT: Dupret, Daniel
 AFFILIANT: Masson, Jean-Michel
 TITLE OF INVENTION: Polynucleotides
 FILE REFERENCE: 58/063,000/21
 CURRENT APPLICATION NUMBER: US/10/131,175
 CURRENT FILING DATE: 2003-08-07
 NUMBER OF SEQ ID NOS: 10
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 10
 LENGTH: 28
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthesized antisense primer
 US-10-131-175-10

Query Match: 44.7%, Score 13.4, DB 15, Length 25,
 Best Local Similarity: 93.8%, Field No: 1,66+04,
 Matches: 17, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

17 GGGAGAGAGAGATTTGT 3

RESULT 40
 US-09-816-460C-44/c
 Sequence 44, Application US/09/816,460C

RESULT 25
US-10-205-009-81
Sequence 81, Application US/10205009
Publication No. US2003011440A1
GENERAL INFORMATION:
APPLICANT: NEROSCA JANICE, LARRY GOLD, PAUL G. SCHMIDT, CHANIFA
APPLICANT: VARGESE, MICHAEL WILLIS
TITLE OF INVENTION: VASCULAR ENDOTHELIAL SP WITH FACTOR (VEGF) INHIBIT
NUMBER OF INVENTION: ACID LIGAND COMPLEXES
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10205009
FILING DATE: 25 JULY 2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10205009
FILING DATE: 13 MAR 2000
APPLICATION NUMBER: US/10205009
FILING DATE: 17 OCTOBER 1997
APPLICATION NUMBER: US/10205009
FILING DATE: 25 OCTOBER 1996
APPLICATION NUMBER: US/10205009
FILING DATE: 6 JUNE 1997
APPLICATION NUMBER: US/10205009
FILING DATE: 21 JULY 1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 31,215
REFERENCE/AGENT NUMBER: NEROSCA JANICE
TELEPHONE/AGENT INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 81:
SEQUENCE CHARACTERISTICS:
LENGTH: 29
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2' fluoro (2'-F)
FEATURE:
OTHER INFORMATION: modified
FEATURE:
OTHER INFORMATION: Polys are 1' modified 1' OMe modified
OTHER INFORMATION: A full length 1' and 3' end restriction are
OTHER INFORMATION: non-coding region, 2' OH
US-10-205-009-81
Query Match 46.0%, Score 13.8, DB 15, Length 29
Best Local Similarity 70.0%, Freq: 10.1, 1e+04
Matches 12, Conserved 3, Mismatches 2, Indels 0, Gaps 0

Sequence 59, Application US/10205009
Publication No. US2003011440A1
GENERAL INFORMATION:
APPLICANT: NEROSCA JANICE, LARRY GOLD, PAUL G. SCHMIDT, CHANIFA
APPLICANT: VARGESE, MICHAEL WILLIS
TITLE OF INVENTION: VASCULAR ENDOTHELIAL SP WITH FACTOR (VEGF) INHIBIT
NUMBER OF INVENTION: ACID LIGAND COMPLEXES
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10205009
FILING DATE: 25 JULY 2002
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/10205009
FILING DATE: 13 MAR 2000
APPLICATION NUMBER: US/10205009
FILING DATE: 17 OCTOBER 1997
APPLICATION NUMBER: US/10205009
FILING DATE: 25 OCTOBER 1996
APPLICATION NUMBER: US/10205009
FILING DATE: 6 JUNE 1997
APPLICATION NUMBER: US/10205009
FILING DATE: 21 JULY 1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 31,215
REFERENCE/AGENT NUMBER: NEROSCA JANICE
TELEPHONE/AGENT INFORMATION:
TELEPHONE: (303) 793-3433
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2' fluoro (2'-F)
FEATURE:
OTHER INFORMATION: modified
FEATURE:
OTHER INFORMATION: Polys are 1' modified 1' OMe modified
OTHER INFORMATION: A full length 1' and 3' end restriction are
OTHER INFORMATION: non-coding region, 2' OH
US-10-205-009-59
Query Match 46.0%, Score 13.8, DB 15, Length 30
Best Local Similarity 70.0%, Freq: 10.1, 1e+04
Matches 12, Conserved 3, Mismatches 2, Indels 0, Gaps 0

0Y 6 TGGGAGAGAGGAGATTG 22
||||| ||||| |||||
2b 6 GGGGAGAGAGAGAGATTG 22

RESULT 27
US-09-890-158-55
Sequence 55, Application US/09906158
Publication No. US20030078217A1
GENERAL INFORMATION:
APPLICANT: Brett P. Montia

US-10-205-009-63

Query Match 46.0% Score 13.8; DB 15; Length 28;
 Best Local Similarity 70.6% Pred. No. 1.1e+04;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 6 TGGGCGAGGAGGAAATTTG 22

2b 6 TGGGCGAGGAGGAAATTTG 22

RESULT 21

US-10-205-009-61

Sequence 61, Application US/10205009
 Publication No. US2000114404A1
 GENERAL INFORMATION:
 APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMITT, CHANIFA
 APPLICANT: VARGESE, MICHAEL WILLIS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NUCLEOTIDE
 TITLE OF INVENTION: ACID LIPID COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Fremont Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10205009
 FILING DATE: 21 JULY 2002
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/0114,968

FILING DATE: 13 Mar 2000
 APPLICATION NUMBER: ECT/03/37/18944
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/739,109
 FILING DATE: 26 OCTOBER 1996
 APPLICATION NUMBER: 08/970,920

FILING DATE: 6 JUNE 1997
 APPLICATION NUMBER: 08/970,920
 FILING DATE: 21 JULY 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,416
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 61:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA

FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' flanked (2'-O)
 OTHER INFORMATION: Purines are 2'-O-methyl (2'-OMe, modified)
 OTHER INFORMATION: A in position 15, and 1 in
 OTHER INFORMATION: position 21 and 22, 3' end 3'-UTR, 2' OH

US-10-205-009-61
 Query Match 46.0% Score 13.8; DB 15; Length 28;
 Best Local Similarity 70.6% Pred. No. 1.1e+04;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 6 TGGGCGAGGAGGAAATTTG 22
 1b 6 TGGGCGAGGAGGAAATTTG 21

RESULT 22

US-10-205-009-78

Sequence 78, Application US/10205009
 Publication No. US2000114404A1
 GENERAL INFORMATION:
 APPLICANT: NEBOJSA JANJIC, LARRY GOLD, PAUL G. SCHMITT, CHANIFA
 APPLICANT: VARGESE, MICHAEL WILLIS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NUCLEOTIDE
 TITLE OF INVENTION: ACID LIPID COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Fremont Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10205009
 FILING DATE: 25 JULY 2002
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/0114,968

FILING DATE: 13 Mar 2000
 APPLICATION NUMBER: ECT/03/37/18944
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/739,109
 FILING DATE: 26 OCTOBER 1996
 APPLICATION NUMBER: 08/970,920

FILING DATE: 6 JUNE 1997
 APPLICATION NUMBER: 08/970,920
 FILING DATE: 21 JULY 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,416
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA

FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' flanked (2'-O)
 OTHER INFORMATION: Purines are 2'-O-methyl (2'-OMe, modified)
 OTHER INFORMATION: A in position 15, and 1 in
 OTHER INFORMATION: position 21 and 22, 3' end 3'-UTR, 2' OH

US-10-205-009-78
 Query Match 46.0% Score 13.8; DB 15; Length 28;
 Best Local Similarity 70.6% Pred. No. 1.1e+04;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

LENGTH: 22
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: PCR Primer
 US-09-066-158 4

Query Match 46.7%, Score 14, E-12, Length 22
 Best Local Similarity 77.3%, Pred. No. 8.6e+03;
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

CY 3 ATTGGGCGAGGATTTCTG 24
 |||||
 22 AGTGGGAGGAGATTTGCT 1

RESULT 18
 US-09-863-830-137/C
 Sequence 137, Application US/09653830
 Patent No. US20020107188A1

GENERAL INFORMATION:
 APPLICANT: Vardach, Arthur A.
 TITLE OF INVENTION: Methods of Identifying and Modulating
 TIME OF INVENTION: 1998-09-18
 FILE REFERENCE: P-10 4794
 CURRENT APPLICATION NUMBER: US/09-863-830-137
 NUMBER OF SEQ. ID NOS: 184
 SOFTWARE: FASTCG for Windows Version 1.0
 SEQ. ID NO. 137
 LENGTH: 24
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-863-830-137

Query Match 46.7%, Score 14, E-12, Length 24
 Best Local Similarity 77.3%, Pred. No. 8.7e+03;
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

CY 7 GCGGCGAGGATTTCTG 28
 |||||
 22 GGTGGGAGGATTTGCTG 1

RESULT 19
 US-10-095-672A-74/C
 Sequence 74, Application US/10095672A
 Patent No. US20020107188A1

GENERAL INFORMATION:
 APPLICANT: Herndon, Thierry
 APPLICANT: Titled, Private
 APPLICANT: Roman-Roman, Sergio
 APPLICANT: Ferrell, Laurent
 TITLE OF INVENTION: METHOD OF IDENTIFYING AND MODULATING
 TIME OF INVENTION: 1998-09-18
 FILE REFERENCE: P-10 4794
 CURRENT APPLICATION NUMBER: US/10-095-672A-74/C
 NUMBER OF SEQ. ID NOS: 184
 SOFTWARE: FASTCG for Windows Version 1.0
 SEQ. ID NO. 74
 LENGTH: 24
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-10-095-672A-74/C

SEQ. ID NO. 74
 LENGTH: 24
 TYPE: DNA
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc feature
 OTHER INFORMATION: Type V Alpha 13
 US-10-095-672A-74

Query Match 46.7%, Score 14, E-12, Length 24
 Best Local Similarity 77.3%, Pred. No. 8.7e+03;
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0

CY 7 GCGGCGAGGATTTCTG 28
 |||||
 22 GGTGGGAGGATTTGCTG 1

RESULT 20
 US-10-205-009-60
 Sequence 60, Application US/100205009
 Patent No. US20020107188A1

GENERAL INFORMATION:
 APPLICANT: HERNDON, THIERRY
 APPLICANT: VARDACH, ARTHUR A.
 APPLICANT: MICHAEL, WILFRIED
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR
 TIME OF INVENTION: 1998-09-18
 NUMBER OF SEQ. ID NOS: 113
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: CO-80140
 COUNTRY: USA
 ZIP: 80111

COMPILED READABLE FORM:
 MODERN TYPE: Diskette, 3.5 inch, 1.44 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10-205-009-60
 FILING DATE: 25-JULY-2002

CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/10-205-009-60
 FILING DATE: 11-MAR-2002

APPLICATION NUMBER: US/10-205-009-60
 FILING DATE: 11-MAR-2002
 APPLICATION NUMBER: US/10-205-009-60
 FILING DATE: 11-OCTOBER-1997
 APPLICATION NUMBER: US/10-205-009-60
 FILING DATE: 25-OCTOBER-1996
 APPLICATION NUMBER: US/10-205-009-60
 FILING DATE: 6-JUNE-1997
 APPLICATION NUMBER: US/10-205-009-60
 FILING DATE: 21-JUNE-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: BARRY C. SWANSON
 REGISTRATION NUMBER: 33,215
 REFERENCE/AGENT NUMBER: NEWELL/NOT 02
 TELEPHONE/MAIL INFORMATION:
 TELEPHONE: (303) 791-3433
 TELEFAX: (303) 791-3433
 INFORMATION FOR SEQ. ID NO.: 60:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MODIFIABLE Y/N: N/A
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' fluorine 2' F
 OTHER INFORMATION: modified

TYPE: DNA
OF INVENTION: HUMAN
US-10-060-830-532

Query Match 48.0% Score 14.4 PB 15 Length 25
Best Local Similarity 48.0% Pct 100.0/0.0
Matches 15 Conservative 0 Mismatches 1 Totals 0 Type 0

9 GGTAGAGAGATTTGTT 24
DB 8 GGTAGAGAGATTTGTT 24

RESULT 7
US-10-060-830-530
Sequence 530, Application US/10060830
Publication No. US2001003154A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong

TITLE OF INVENTION: HUMAN LECT HOMAN CONTAINING PROTEIN
FILE REFERENCE: PB0169
CURRENT APPLICATION NUMBER: US/10/060,830
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,762
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 1123
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 530
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-060-830-530

Query Match 48.0% Score 14.4 PB 15 Length 25
Best Local Similarity 48.0% Pct 100.0/0.0
Matches 15 Conservative 0 Mismatches 1 Totals 0 Type 0

9 GGTAGAGAGATTTGTT 24
DB 8 GGTAGAGAGATTTGTT 23

RESULT 8
US-10-060-830-531
Sequence 531, Application US/10060830
Publication No. US2001003154A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
TITLE OF INVENTION: HUMAN LECT HOMAN CONTAINING PROTEIN
FILE REFERENCE: PB0169
CURRENT APPLICATION NUMBER: US/10/060,830
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669

PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,762
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 1123
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 531
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-060-830-531

Query Match 48.0% Score 14.4 PB 15 Length 25
Best Local Similarity 48.0% Pct 100.0/0.0
Matches 15 Conservative 0 Mismatches 1 Totals 0 Type 0

9 GGTAGAGAGATTTGTT 24
DB 7 GGTAGAGAGATTTGTT 22

RESULT 9
US-10-060-830-532
Sequence 532, Application US/10060830
Publication No. US2001003154A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
TITLE OF INVENTION: HUMAN LECT HOMAN CONTAINING PROTEIN
FILE REFERENCE: PB0169
CURRENT APPLICATION NUMBER: US/10/060,830
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,761
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 09/864,762
PRIOR FILING DATE: 2001-01-30
NUMBER OF SEQ ID NOS: 1123
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 532
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapiens
US-10-060-830-532

Query Match 48.0% Score 14.4 PB 15 Length 25
Best Local Similarity 48.0% Pct 100.0/0.0
Matches 15 Conservative 0 Mismatches 1 Totals 0 Type 0

9 GGTAGAGAGATTTGTT 24
DB 6 GGTAGAGAGATTTGTT 21

RESULT 10
US-10-060-830-533
Sequence 533, Application US/10060830
Publication No. US2001003154A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
TITLE OF INVENTION: HUMAN LECT HOMAN CONTAINING PROTEIN
FILE REFERENCE: PB0169
CURRENT APPLICATION NUMBER: US/10/060,830
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669

PUBLICATION INFORMATION:
Publication No. H080603063215441
GENERAL INFORMATION:
APPLICANT: GU, Yizhong
AFFILIANT: Nanyang, Sui-Tung
TITLE OF INVENTION: HUMAN 197L TOWAN CONTAINING PROTEIN
FILE REFERENCE: P00159
CURRENT AFFILIATION NUMBER: 021-10000-430
CURRENT FILING DATE: 2003-01-30
PRIORITY FILING DATE: 2003-01-30
PRIORITY FILING NUMBER: 100-2000-00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY FILING NUMBER: 127/US01/009664
PRIOR FILING DATE: 2001-01-30
PRIOR FILING NUMBER: 100-2000-00668
PRIOR FILING DATE: 2001-01-30
PRIOR FILING NUMBER: 127/US01/009665
PRIOR FILING DATE: 2001-01-30

PRINTED DATE: 2001-01-30
 FROM: ALLIANCE FOR THE 2003
 ELECTIONS
 FROM: 2001-01-30

1 PRIOR FILING DATE: 2001-05-23
 2 PRIOR APPLICATION NUMBER: US 60/325,062
 3 PRIOR FILING DATE: 2001-09-25

```

1 SEQ ID NO 528
2
3 LENGTH: 25
4
5
6

```

TITLE: DNA
Occurrence: Homo sapiens
DS-10-000-00-228

Query Match	46.03	Score 14.4	Dh 15	Length 15
Best Local Similarity	93.83	Pred. No. 5.9e+03		
Matches 15	Conservative	0	Mismatches 1	Index 0
				Days 0

[illegible]

RESULT 6

Publication No. US20030032154A1
GENERAL INFORMATION
APPLICANT: Gu, Hzhong
ATTORNEY: Hunter, David Thomas

TABLE OF JEWELRY, HOWARD DILL EXHIBIT CONTINUING FROM
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 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: 21/US01/00064
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696	11	36.7	125	10	10	Sequence 15585, A
697	11	36.7	125	10	10	Sequence 15586, A
698	11	36.7	125	10	10	Sequence 15587, A
699	11	36.7	125	10	10	Sequence 15588, A
700	11	36.7	125	10	10	Sequence 15589, A

182	11.4	38.0	2.9	19	US-10-094-263B-1753	Sequence 157, Ap
183	11.4	38.0	2.9	19	US-10-094-263B-1754	Sequence 158, Ap
184	11.4	38.0	2.9	19	US-10-094-263B-1755	Sequence 159, Ap
185	11.4	38.0	2.9	19	US-10-094-263B-1756	Sequence 160, Ap
186	11.4	38.0	2.9	19	US-10-094-263B-1757	Sequence 161, Ap
187	11.4	38.0	2.9	19	US-10-094-263B-1758	Sequence 162, Ap
188	11.4	38.0	2.9	19	US-10-094-263B-1759	Sequence 163, Ap
189	11.4	38.0	2.9	19	US-10-094-263B-1760	Sequence 164, Ap
190	11.4	38.0	2.9	19	US-10-094-263B-1761	Sequence 165, Ap
191	11.4	38.0	2.9	19	US-10-094-263B-1762	Sequence 166, Ap
192	11.4	38.0	2.9	19	US-10-094-263B-1763	Sequence 167, Ap
193	11.4	38.0	2.9	19	US-10-094-263B-1764	Sequence 168, Ap
194	11.4	38.0	2.9	19	US-10-094-263B-1765	Sequence 169, Ap
195	11.4	38.0	2.9	19	US-10-094-263B-1766	Sequence 170, Ap
196	11.4	38.0	2.9	19	US-10-094-263B-1767	Sequence 171, Ap
197	11.4	38.0	2.9	19	US-10-094-263B-1768	Sequence 172, Ap
198	11.4	38.0	2.9	19	US-10-094-263B-1769	Sequence 173, Ap
199	11.4	38.0	2.9	19	US-10-094-263B-1770	Sequence 174, Ap
200	11.4	38.0	2.9	19	US-10-094-263B-1771	Sequence 175, Ap
201	11.4	38.0	2.9	19	US-10-094-263B-1772	Sequence 176, Ap
202	11.4	38.0	2.9	19	US-10-094-263B-1773	Sequence 177, Ap
203	11.4	38.0	2.9	19	US-10-094-263B-1774	Sequence 178, Ap
204	11.4	38.0	2.9	19	US-10-094-263B-1775	Sequence 179, Ap
205	11.4	38.0	2.9	19	US-10-094-263B-1776	Sequence 180, Ap
206	11.4	38.0	2.9	19	US-10-094-263B-1777	Sequence 181, Ap
207	11.4	38.0	2.9	19	US-10-094-263B-1778	Sequence 182, Ap
208	11.4	38.0	2.9	19	US-10-094-263B-1779	Sequence 183, Ap
209	11.4	38.0	2.9	19	US-10-094-263B-1780	Sequence 184, Ap
210	11.4	38.0	2.9	19	US-10-094-263B-1781	Sequence 185, Ap
211	11.4	38.0	2.9	19	US-10-094-263B-1782	Sequence 186, Ap
212	11.4	38.0	2.9	19	US-10-094-263B-1783	Sequence 187, Ap
213	11.4	38.0	2.9	19	US-10-094-263B-1784	Sequence 188, Ap
214	11.4	38.0	2.9	19	US-10-094-263B-1785	Sequence 189, Ap
215	11.4	38.0	2.9	19	US-10-094-263B-1786	Sequence 190, Ap
216	11.4	38.0	2.9	19	US-10-094-263B-1787	Sequence 191, Ap
217	11.4	38.0	2.9	19	US-10-094-263B-1788	Sequence 192, Ap
218	11.4	38.0	2.9	19	US-10-094-263B-1789	Sequence 193, Ap
219	11.4	38.0	2.9	19	US-10-094-263B-1790	Sequence 194, Ap
220	11.4	38.0	2.9	19	US-10-094-263B-1791	Sequence 195, Ap
221	11.4	38.0	2.9	19	US-10-094-263B-1792	Sequence 196, Ap
222	11.4	38.0	2.9	19	US-10-094-263B-1793	Sequence 197, Ap
223	11.4	38.0	2.9	19	US-10-094-263B-1794	Sequence 198, Ap
224	11.4	38.0	2.9	19	US-10-094-263B-1795	Sequence 199, Ap
225	11.4	38.0	2.9	19	US-10-094-263B-1796	Sequence 200, Ap
226	11.4	38.0	2.9	19	US-10-094-263B-1797	Sequence 201, Ap
227	11.4	38.0	2.9	19	US-10-094-263B-1798	Sequence 202, Ap
228	11.4	38.0	2.9	19	US-10-094-263B-1799	Sequence 203, Ap
229	11.4	38.0	2.9	19	US-10-094-263B-1800	Sequence 204, Ap
230	11.4	38.0	2.9	19	US-10-094-263B-1801	Sequence 205, Ap
231	11.4	38.0	2.9	19	US-10-094-263B-1802	Sequence 206, Ap
232	11.4	38.0	2.9	19	US-10-094-263B-1803	Sequence 207, Ap
233	11.4	38.0	2.9	19	US-10-094-263B-1804	Sequence 208, Ap
234	11.4	38.0	2.9	19	US-10-094-263B-1805	Sequence 209, Ap
235	11.4	38.0	2.9	19	US-10-094-263B-1806	Sequence 210, Ap
236	11.4	38.0	2.9	19	US-10-094-263B-1807	Sequence 211, Ap
237	11.4	38.0	2.9	19	US-10-094-263B-1808	Sequence 212, Ap
238	11.4	38.0	2.9	19	US-10-094-263B-1809	Sequence 213, Ap
239	11.4	38.0	2.9	19	US-10-094-263B-1810	Sequence 214, Ap
240	11.4	38.0	2.9	19	US-10-094-263B-1811	Sequence 215, Ap
241	11.4	38.0	2.9	19	US-10-094-263B-1812	Sequence 216, Ap
242	11.4	38.0	2.9	19	US-10-094-263B-1813	Sequence 217, Ap
243	11.4	38.0	2.9	19	US-10-094-263B-1814	Sequence 218, Ap
244	11.4	38.0	2.9	19	US-10-094-263B-1815	Sequence 219, Ap
245	11.4	38.0	2.9	19	US-10-094-263B-1816	Sequence 220, Ap
246	11.4	38.0	2.9	19	US-10-094-263B-1817	Sequence 221, Ap
247	11.4	38.0	2.9	19	US-10-094-263B-1818	Sequence 222, Ap
248	11.4	38.0	2.9	19	US-10-094-263B-1819	Sequence 223, Ap
249	11.4	38.0	2.9	19	US-10-094-263B-1820	Sequence 224, Ap
250	11.4	38.0	2.9	19	US-10-094-263B-1821	Sequence 225, Ap
251	11.4	38.0	2.9	19	US-10-094-263B-1822	Sequence 226, Ap
252	11.4	38.0	2.9	19	US-10-094-263B-1823	Sequence 227, Ap
253	11.4	38.0	2.9	19	US-10-094-263B-1824	Sequence 228, Ap
254	11.4	38.0	2.9	19	US-10-094-263B-1825	Sequence 229, Ap
255	11.4	38.0	2.9	19	US-10-094-263B-1826	Sequence 230, Ap
256	11.4	38.0	2.9	19	US-10-094-263B-1827	Sequence 231, Ap
257	11.4	38.0	2.9	19	US-10-094-263B-1828	Sequence 232, Ap
258	11.4	38.0	2.9	19	US-10-094-263B-1829	Sequence 233, Ap
259	11.4	38.0	2.9	19	US-10-094-263B-1830	Sequence 234, Ap
260	11.4	38.0	2.9	19	US-10-094-263B-1831	Sequence 235, Ap
261	11.4	38.0	2.9	19	US-10-094-263B-1832	Sequence 236, Ap
262	11.4	38.0	2.9	19	US-10-094-263B-1833	Sequence 237, Ap
263	11.4	38.0	2.9	19	US-10-094-263B-1834	Sequence 238, Ap
264	11.4	38.0	2.9	19	US-10-094-263B-1835	Sequence 239, Ap
265	11.4	38.0	2.9	19	US-10-094-263B-1836	Sequence 240, Ap
266	11.4	38.0	2.9	19	US-10-094-263B-1837	Sequence 241, Ap
267	11.4	38.0	2.9	19	US-10-094-263B-1838	Sequence 242, Ap
268	11.4	38.0	2.9	19	US-10-094-263B-1839	Sequence 243, Ap
269	11.4	38.0	2.9	19	US-10-094-263B-1840	Sequence 244, Ap
270	11.4	38.0	2.9	19	US-10-094-263B-1841	Sequence 245, Ap
271	11.4	38.0	2.9	19	US-10-094-263B-1842	Sequence 246, Ap
272	11.4	38.0	2.9	19	US-10-094-263B-1843	Sequence 247, Ap
273	11.4	38.0	2.9	19	US-10-094-263B-1844	Sequence 248, Ap
274	11.4	38.0	2.9	19	US-10-094-263B-1845	Sequence 249, Ap
275	11.4	38.0	2.9	19	US-10-094-263B-1846	Sequence 250, Ap
276	11.4	38.0	2.9	19	US-10-094-263B-1847	Sequence 251, Ap
277	11.4	38.0	2.9	19	US-10-094-263B-1848	Sequence 252, Ap
278	11.4	38.0	2.9	19	US-10-094-263B-1849	Sequence 253, Ap
279	11.4	38.0	2.9	19	US-10-094-263B-1850	Sequence 254, Ap
280	11.4	38.0	2.9	19	US-10-094-263B-1851	Sequence 255, Ap
281	11.4	38.0	2.9	19	US-10-094-263B-1852	Sequence 256, Ap
282	11.4	38.0	2.9	19	US-10-094-263B-1853	Sequence 257, Ap
283	11.4	38.0	2.9	19	US-10-094-263B-1854	Sequence 258, Ap
284	11.4	38.0	2.9	19	US-10-094-263B-1855	Sequence 259, Ap
285	11.4	38.0	2.9	19	US-10-094-263B-1856	Sequence 260, Ap
286	11.4	38.0	2.9	19	US-10-094-263B-1857	Sequence 261, Ap
287	11.4	38.0	2.9	19	US-10-094-263B-1858	Sequence 262, Ap
288	11.4	38.0	2.9	19	US-10-094-263B-1859	Sequence 263, Ap
289	11.4	38.0	2.9	19	US-10-094-263B-1860	Sequence 264, Ap
290	11.4	38.0	2.9	19	US-10-094-263B-1861	Sequence 265, Ap
291	11.4	38.0	2.9	19	US-10-094-263B-1862	Sequence 266, Ap
292	11.4	38.0	2.9	19	US-10-094-263B-1863	Sequence 267, Ap
293	11.4	38.0	2.9	19	US-10-094-263B-1864	Sequence 268, Ap
294	11.4	38.0	2.9	19	US-10-094-263B-1865	Sequence 269, Ap
295	11.4	38.0	2.9	19	US-10-094-263B-1866	Sequence 270, Ap
296	11.4	38.0	2.9	19	US-10-094-263B-1867	Sequence 271, Ap
297	11.4	38.0	2.9	19	US-10-094-263B-1868	Sequence 272, Ap
298	11.4	38.0	2.9	19	US-10-094-263B-1869	Sequence 273, Ap
299	11.4	38.0	2.9	19	US-10-094-263B-1870	Sequence 274, Ap
300	11.4	38.0	2.9	19	US-10-094-263B-1871	Sequence 275, Ap
301	11.4	38.0	2.9	19	US-10-094-263B-1872	Sequence 276, Ap
302	11.4	38.0	2.9	19	US-10-094-263B-1873	Sequence 277, Ap
303	11.4	38.0	2.9	19	US-10-094-263B-1874	Sequence 278, Ap
304	11.4	38.0	2.9	19	US-10-094-263B-1875	Sequence 279, Ap
305	11.4	38.0	2.9	19	US-10-094-263B-1876	Sequence 280, Ap
306	11.4	38.0	2.9	19	US-10-094-263B-1877	Sequence 281, Ap
307	11.4	38.0	2.9	19	US-10-094-263B-1878	Sequence 282, Ap
308	11.4	38.0	2.9	19	US-10-094-263B-1879	Sequence 283, Ap
309	11.4	38.0	2.9	19	US-10-094-263B-1880	Sequence 284, Ap
310	11.4	38.0	2.9	19	US-10-094-263B-1881	Sequence 285, Ap
311	11.4	38.0	2.9	19	US-10-094-263B-1882	Sequence 286, Ap
312	11.4	38.0	2.9	19	US-10-094-263B-1883	Sequence 287, Ap
313	11.4	38.0	2.9	19	US-10-094-263B-1884	Sequence 288, Ap
314	11.4	38.0	2.9	19	US-10-094-263B-1885	Sequence 289, Ap
315	11.4	38.0	2.9	19	US-10-094-263B-1886	Sequence 290, Ap
316	11.4	38.0	2.9	19	US-10-094-263B-1887	Sequence 291, Ap
317	11.4	38.0	2.9	19	US-10-094-263B-1888	Sequence 292, Ap
318	11.4	38.0	2.9	19	US-10-094-263B-1889	Sequence 293, Ap
319	11.4	38.0	2.9	19	US-10-094-263B-1890	Sequence 294, Ap
320	11.4	38.0	2.9	19	US-10-094-263B-1891	Sequence 295, Ap
321	11.4	38.0	2.9	19	US-10-094-263B-1892	Sequence 296, Ap
322	11.4	38.0	2.9	19	US-10-094-263B-1893	Sequence 297, Ap
323	11.4	38.0	2.9	19	US-10-094-263B-1894	Sequence 298, Ap
324	11.4	38.0	2.9	19	US-10-094-263B-1895	Sequence 299, Ap
325	11.4	38.0	2.9	19	US-10-094-263B-1896	Sequence 300, Ap
326	11.4	38.0	2.9	19	US-10-094-263B-1897	Sequence 301, Ap
327	11.4	38.0	2.9	19	US-10-094-263B-1898	Sequence 302, Ap
328	11.4	38.0	2.9	19	US-10-094-263B-1899	Sequence 303, Ap
329	11.4	38.0	2.9	19	US-10-094-263B-1900	Sequence 304, Ap
330	11.4	38.0	2.9	19	US-10-094-263B-1901	Sequence 305, Ap
331	11.4	38.0	2.9	19	US-10-094-263B-1902	Sequence 306, Ap
332	11.4	38.0	2.9	19	US-10-094-263B-1903	Sequence 307, Ap
333	11.4	38.0	2.9	19	US-10-094-263B-1904	Sequence 308, Ap
334	11.4	38.0	2.9	19	US-10-094-263B-1905	Sequence 309, Ap
335	11.4	38.0	2.9	19	US-10-094-263B-1906	Sequence 310, Ap
336	11.4	38.0	2.9	19	US-10-094-263B-190	

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90	12.4	41.3	17	15	US-10-060-830-450	Sequence 23, Aff	0.162	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
91	12.4	41.3	20	15	US-10-060-830-450	Sequence 34, Aff	0.164	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
92	12.4	41.3	22	15	US-10-060-830-450	Sequence 39, Aff	0.165	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
93	12.4	41.3	25	15	US-10-060-830-450	Sequence 47, Aff	0.167	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
94	12.4	41.3	26	15	US-10-060-830-450	Sequence 54, Aff	0.168	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
95	12.4	41.3	27	15	US-10-060-830-450	Sequence 59, Aff	0.169	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
96	12.4	41.3	28	15	US-10-060-830-450	Sequence 64, Aff	0.170	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
97	12.4	41.3	29	15	US-10-060-830-450	Sequence 69, Aff	0.171	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
98	12.4	41.3	30	15	US-10-060-830-450	Sequence 74, Aff	0.172	11.9	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
99	12.4	41.3	31	15	US-09-801-274-191	Sequence 110, Aff	0.173	11.8	32.2	25	15	US-09-944-403-72	Sequence 72, Aff
100	12.4	41.3	32	15	US-09-801-274-191	Sequence 111, Aff	0.174	11.8	32.2	25	15	US-09-944-403-72	Sequence 72, Aff
101	12.4	41.3	34	15	US-09-801-274-191	Sequence 112, Aff	0.175	11.8	32.2	25	15	US-09-944-403-72	Sequence 72, Aff
102	12.4	40.7	17	11	US-09-854-785-176	Sequence 63, Aff	0.176	11.8	32.2	25	15	US-09-944-403-72	Sequence 72, Aff
103	12.4	40.7	17	11	US-09-854-785-176	Sequence 170, Aff	0.176	11.8	32.2	25	15	US-09-944-403-72	Sequence 72, Aff
104	12.4	40.7	20	15	US-10-001-076-794	Sequence 14, Aff	0.178	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
105	12.4	40.7	20	15	US-10-001-076-794	Sequence 94, Aff	0.178	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
106	12.4	40.7	21	15	US-10-001-076-794	Sequence 94, Aff	0.179	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
107	12.2	40.7	22	11	US-09-944-403-72	Sequence 84, Aff	0.180	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
108	12.2	40.7	22	11	US-09-944-403-72	Sequence 144, Aff	0.181	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
109	12.2	40.7	22	15	US-10-137-251-77	Sequence 7, Aff	0.182	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
110	12.2	40.7	25	15	US-09-944-403-72	Sequence 139, Aff	0.183	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
111	12.2	40.7	25	15	US-10-000-000-000	Sequence 126, Aff	0.184	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
112	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
113	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
114	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
115	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
116	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
117	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
118	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
119	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
120	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
121	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
122	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
123	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
124	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
125	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
126	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
127	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
128	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
129	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
130	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
131	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
132	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
133	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
134	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
135	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
136	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
137	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
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139	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
140	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
141	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
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146	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
147	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
148	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
149	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
150	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff
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152	12.2	40.7	25	15	US-10-000-000-000	Sequence 139, Aff	0.185	11.8	32.3	25	15	US-09-944-403-72	Sequence 72, Aff

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ON NUCLEAR-INDUCED SCORCH, ARISING ON POLY-

[illegible]

Flt Lt: 1944-1945

Sequence: 1 gtaattcggcagaggaat+g++g+g+ 20

Conclusions

GAFFNEY, J. J. 1971. The ecology of the San Joaquin River delta, California. *California Fish and Game* 57:1-14.

Searched: 1439767 2075, 107100076 1771776

Total number of hits satisfying 9-sec criterion: 7497

Maximum DE seq length: 0

Abstract

THE UNIVERSITY OF CHICAGO

Maximum Match 10

LIST OF REFERENCES

Database : Published Applications WA:

Result No.	Score	Query Match	Length	ES	ID	Description
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2	15	50.0	24	15	CG05-000-2200-14	Segment 14, All
3	14.4	48.0	17	15	CG05-000-2200-15	Segment 15, All
4	14.4	48.0	17	15	CG05-000-2200-16	Segment 16, All
5	14.4	48.0	17	15	CG05-000-2200-17	Segment 17, All
6	14.4	48.0	17	15	CG05-000-2200-18	Segment 18, All
7	14.4	48.0	17	15	CG05-000-2200-19	Segment 19, All
8	14.4	48.0	25	15	CG05-000-2200-20	Segment 20, All

Red. No. in the number of votes for protection by printing a score greater than or equal to the average, by being being printed and is being by analysis of the total number of votes.

SUMMARY

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2	44.5	50.0	24	12	100	Sequence 1377, A
3	44.4	49.0	17	15	100	Sequence 1377, A
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9	44.4	48.0	23	15	100	Sequence 1377, A
10	44.4	48.0	23	15	100	Sequence 1377, A
11	44.4	48.0	23	15	100	Sequence 1377, A
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13	44.4	48.0	23	15	100	Sequence 1377, A
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17	44.4	48.0	23	15	100	Sequence 1377, A
18	44.4	48.0	23	15	100	Sequence 1377, A
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21	44.4	48.0	23	15	100	Sequence 1377, A
22	44.4	48.0	23	15	100	Sequence 1377, A
23	44.4	48.0	23	15	100	Sequence 1377, A
24	44.4	48.0	23	15	100	Sequence 1377, A
25	44.4	48.0	23	15	100	Sequence 1377, A
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54	44.4	48.0	23	15	100	Sequence 1377, A
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87	44.4	48.0	23	15	100	Sequence 1377, A
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91	44.4	48.0	23	15	100	Sequence 1377, A
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100	44.4	48.0	23	15	100	Sequence 1377, A

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: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (212) 278-1000
: TELEFAX: (212) 953-7249
: INFORMATION FOR SEQ ID NO: 14:
:   SOURCE CHARACTERISTICS:
:     LENGTH: 30 bases
:     TYPE: nucleic acid
:     STRAIGHTNESS: single
:     TOPOLOGY: linear
:     MOLECULE TYPE: oligonucleotide DNA
: US-08-353-761-14

Query Match      43.3%; Score 13; DB 1; Length 30;
Best Local Similarity 76.2%; Pred. No. 2.5e+03;
Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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30  GGCACGAGTCAGCTCTTCACT 29

Search completed: July 21, 2003, 15:48:55
Job time : 30.994 secs
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APPLICANT: CHUNG, Bong Hyun
APPLICANT: NAM, Soo Wan
APPLICANT: KIM, Byung Moon
APPLICANT: YANG, Sun Ah
APPLICANT: PARK, Young Hoon
TITLE OF INVENTION: SIGNAL SEQUENCES FOR SECRETION
TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS FROM
TITLE OF INVENTION: YEAST
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHUNG, Bong Hyun
STREET: Hanwool Apt. 101-702, Shinsung-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-345
ADDRESSEE: NAM, Soo Wan
STREET: Hanwool Apt. 101-702, Shinsung-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-345
ADDRESSEE: KIM, Byung Moon
STREET: 53-2, Bokdal-dong
CITY: Cheongju-si
STATE: Chungcheongbuk-do
COUNTRY: Republic of Korea
ZIP: 360-270
ADDRESSEE: YANG, Sun Ah
STREET: 626-10, Shinsung-1-dong,
STREET: Dong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: PARK, Young Hoon
STREET: Town House 5-101, 391, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-340
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25inch, 1.44M storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 2006/353,751
FILING DATE: 12-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 93 27269
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER: A 9803
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-1000
TELEFAX: (212) 278-1000
INFORMATION FOR SEQ. ID NO. 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30 bases
TYPE: nucleic acid
STRANDS: single
TOPOLOGY: linear
MOLECULE TYPE: oligonucleotide
US-09-353-751-9
Query Match 43.3% Score 13, DB 1, Length 30

Best Local Similarity 76%, Field No. 2, Dec 93
Matches 16, Conservative 0, Mismatch 6, Indels 7, Gap 0
C7 9 GCGAGCGAGATCTTTT 29
DB 28 GCGAGCGAGATCTTTT 8
RESULT 40
US-09-353-751-14
Sequence 14, Application US/09353751
Patent No. 5712113
GENERAL INFORMATION:
APPLICANT: CHUNG, Bong Hyun
APPLICANT: NAM, Soo Wan
APPLICANT: KIM, Byung Moon
APPLICANT: YANG, Sun Ah
APPLICANT: PARK, Young Hoon
TITLE OF INVENTION: SIGNAL SEQUENCES FOR SECRETION
TITLE OF INVENTION: OF HETEROLOGOUS PROTEINS FROM
TITLE OF INVENTION: YEAST
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHUNG, Bong Hyun
STREET: Hanwool Apt. 101-702, Shinsung-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-345
ADDRESSEE: NAM, Soo Wan
STREET: Hanwool Apt. 101-702, Shinsung-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: KIM, Byung Moon
STREET: 53-2, Bokdal-dong
CITY: Cheongju-si
STATE: Chungcheongbuk-do
COUNTRY: Republic of Korea
ZIP: 360-270
ADDRESSEE: YANG, Sun Ah
STREET: 626-10, Shinsung-1-dong,
STREET: Dong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-340
ADDRESSEE: PARK, Young Hoon
STREET: Town House 5-101, 391, Doryong-dong,
STREET: Yuseong-gu
CITY: Daejeon
STATE:
COUNTRY: Republic of Korea
ZIP: 305-340
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25inch, 1.44M storage
COMPUTER: IBM PC/AT
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 2006/353,751
FILING DATE: 12-DEC-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: KR 93 27269
FILING DATE: 10-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Shahan Islam
REGISTRATION NUMBER: 32,507
REFERENCE/DOCKET NUMBER: A 9803

FILE REFERENCE: 232-134
 CURRENT APPLICATION NUMBER: US/09/177,650
 CURRENT FILING DATE: 1998-10-23
 EARLIER APPLICATION NUMBER: 07/063,147
 EARLIER FILING DATE: 1997-10-24
 NUMBER OF SEQ ID NOS: 129
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 58
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-177-650-58

Query Match 41.0% Score 13.0 DB 4 Length 25
 Best Local Similarity 76.0% Freq. No. 2,49+03
 Matches 15, Conservative 0, Mismatches 1, Indels 0, Gaps 0

CY 1 GTATTGGCGGAGGGA 18
 5 GTTCTGGCGGAGGAGGA 20

RESULT 34
 US-09-656-952-5/C
 Sequence 5, Affiliation: us-09-656-952
 Patent No. 6444443
 GENERAL INFORMATION:
 APPLICANT: Gaber, Jared et al.
 TITLE OF INVENTION: No. 6444443-1 Gene
 CURRENT APPLICATION NUMBER: US/09/177,650
 CURRENT FILING DATE: 1998-10-23
 NUMBER OF SEQ ID NOS: 20
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO 5
 LENGTH: 22
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-656-952-5

Query Match 43.3% Score 13.0 DB 4 Length 22
 Best Local Similarity 76.0% Freq. No. 2,49+03
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Gaps 0

CY 9 GGCAGGAGGAGTGTGTGT 29
 22 GGCAGGAGGAGTGTGTGT 2

RESULT 35
 US-09-584-040-1163/C
 Sequence 1163, Affiliation: us-09-584-040-1163
 Patent No. 6346194
 GENERAL INFORMATION:
 APPLICANT: Hsu, Feng
 APPLICANT: Mosiggen, James
 APPLICANT: Olinchick, Dan T.
 APPLICANT: Rappaport, Yair
 TITLE OF INVENTION: METHOD AND REAGENT FOR THE
 TITLE OF INVENTION: TREATMENT OF DISEASES VIA
 TITLE OF INVENTION: CONDITION RELATED TO LEVELS
 TITLE OF INVENTION: OF VARIOUS ENZYME ACTIVITY
 TITLE OF INVENTION: GROWTH FACTOR
 NUMBER OF SEQ ID NOS: 673
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: LYON & LYON
 STREET: 613 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071-2066
 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: Storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM PC, DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/584,040
 FILING DATE: January 11, 1996
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 63/066,974
 FILING DATE: October 26, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Warburg, Richard J.
 REGISTRATION NUMBER: 30,127
 REFERENCE/DESKET NUMBER: 09/18,964
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 673510
 INFORMATION FOR SEQ ID NO: 1163:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 27 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 FEATURE:
 OTHER INFORMATION: The letter "N" represents the stem 11 region
 US-09-584-040-1163

Query Match 41.0% Score 13.0 DB 4 Length 27
 Best Local Similarity 76.0% Freq. No. 2,49+03
 Matches 16, Conservative 0, Mismatches 6, Indels 0, Gaps 0

CY 3 AATPCCGAGGAGGAGTGT 24
 22 AATPCCGAGGAGGAGTGT 1

RESULT 36
 US-09-040-725A-3
 Sequence 3, Affiliation: us-09-040-725A-3
 Patent No. 6399584
 GENERAL INFORMATION:
 APPLICANT: Institut Curie
 APPLICANT: CNRS
 APPLICANT: Arpin, Monique
 APPLICANT: Cepaldi, Tiziana
 APPLICANT: Gautreau, Alexis
 APPLICANT: Lovaard, Daniel
 TITLE OF INVENTION: Pharmacological compounds which act on the
 TITLE OF INVENTION: on tyrosine 353
 FILE REFERENCE: 33/083,001/00
 CURRENT APPLICATION NUMBER: US/09/040,725A
 CURRENT FILING DATE: 1998-03-18
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 3
 LENGTH: 29
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-040-725A-3

Query Match 43.3% Score 13.0 DB 4 Length 29
 Best Local Similarity 76.0% Freq. No. 2,50+03
 Matches 16, Conservative 0, Mismatches 5, Indels 0, Gaps 0

CY 1 GTATTGGCGGAGGAGT 21
 1 GTATTGGCGGAGGAGT 21

CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90017
COMPUTER READABLE FORM:
MEDIUM TYPE: 3 1/2 Diskette, 1 44 MB storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/470,887A
FILING DATE: June 2, 1994
CLASSIFICATION:
PRIORITY APPLICATION DATA: including application
PRIORITY APPLICATION DATA: described below:
APPLICATION NUMBER: none
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Waiburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 30,742
TELEPHONE: (213) 955-0440
TELEFAX: (213) 955-0440
TELECOMMUNICATION INFORMATION:
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 31
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
PI: US94-06311A-37

Query Match 44.0% Score 13.2; DB 1; Length 31;
Best Local Similarity 93.3%; Pctd No. 1,660,93;
Matches 14; Conservative 0; Mismatches 0; Gaps 0;

CY 15 AGAAGATTGTTCTGT 29
DB 26 AGAAGATTGTTCTGT 12

SEQID 29
US-08-323 199D 1
Sequence 1: Application US/03031312D
Patent No. 5786199
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXTENSION SYSTEM AND VACCINES
NUMBER OF SEQUENCES: 70
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 05/08/470,887A
FILING DATE: 14-OCT-1994
CLASSIFICATION: 415
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682 035
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 790-9090
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-323 192D-1

Query Match 44.0% Score 13.2; DB 1; Length 31;
Best Local Similarity 43.4%; Pctd No. 1,660,93;
Matches 15; Conservative 0; Mismatches 3; Gaps 0;

CY 12 AGAAGATTGTTCTGT 29
DB 2 AGAAGATTGTTCTGT 19

SEQID 29
US-08-323 192D-1
Sequence 1: Application US/03031312D
Patent No. 5820871
GENERAL INFORMATION:
APPLICANT: Palese, Peter
TITLE OF INVENTION: RECOMBINANT NEGATIVE STRAND RNA VIRUS
TITLE OF INVENTION: EXTENSION SYSTEM AND VACCINES
NUMBER OF SEQUENCES: 60
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,887A
FILING DATE: 06-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Cortuzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7682 036
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 21 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
US-08-323 192D-1

Query Match 44.0% Score 13.2; DB 1; Length 31;
Best Local Similarity 43.4%; Pctd No. 1,660,93;
Matches 15; Conservative 0; Mismatches 3; Gaps 0;

CY 12 AGAAGATTGTTCTGT 29
DB 2 AGAAGATTGTTCTGT 19

MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2' fluoro (2'-F)
modified
SEQUENCE INFORMATION: N of Position 11 is a 3' U linker
deoxythymidine
SEQUENCE INFORMATION: 44-73 to 156
US-09-224-968-59
Query Match 44-73 Score 13.4 DB 4 Length 28
Best Local Similarity 73.0% Field No 1 54-033
Matches 17 Conservative 0 Mismatches 6 Indels 0 Gaps 0
2 TAAATGGAGCAAGGATTTT 24
|||||

US-08 869 998-1356/C
Sequence 1356, Application US/08880998
Patent No. 5994076
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Birkhaskvili, Robert
TITLE OF INVENTION: METHOD OF ADVANCING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/863, 108
FILING DATE: 21-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
PREPPER/COMPT NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ 10 NO. 1356:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-09-859-998-1356
Query Match 44-73 Score 13.4 DB 4 Length 28
Best Local Similarity 73.0% Field No 1 54-033
Matches 17 Conservative 0 Mismatches 6 Indels 0 Gaps 0
2 TAAATGGAGCAAGGATTTT 24
|||||

DB 23 TAAATGGAGCAAGGATTTT 1
RESULT 26
US-09-225 928 1356/C
Patent No. 6352823
GENERAL INFORMATION:
APPLICANT: Chenchik, Alex
APPLICANT: Jokhadze, George
APPLICANT: Birkhaskvili, Robert
TITLE OF INVENTION: METHOD OF ADVANCING DIFFERENTIAL
TITLE OF INVENTION: EXPRESSION
NUMBER OF SEQUENCES: 1375
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 2200 Sand Hill Road, Suite 100
CITY: Menlo Park
STATE: CA
COUNTRY: US
ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/028, 928
FILING DATE: 05-Jan-1999
CLASSIFICATION: unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/863, 098
FILING DATE: 21-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Field, Bret E.
REGISTRATION NUMBER: 37,620
PREPPER/COMPT NUMBER: 08/08/076, 001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-322-5070
TELEFAX: 415-854-0875
INFORMATION FOR SEQ 10 NO. 1356:
SEQUENCE CHARACTERISTICS:
LENGTH: 28 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
FEATURE:
OTHER INFORMATION: oligonucleotide primer
US-09-225 928-1356
Query Match 44-73 Score 13.4 DB 4 Length 28
Best Local Similarity 73.0% Field No 1 54-033
Matches 17 Conservative 0 Mismatches 6 Indels 0 Gaps 0
2 TAAATGGAGCAAGGATTTT 24
DB 23 TAAATGGAGCAAGGATTTT 1
RESULT 27
PCT-US94-06331A-37/C
Sequence 37, Application PCT/US9406331A
GENERAL INFORMATION:
APPLICANT: Ribozyme Pharmaceuticals, Inc.
TITLE OF INVENTION: METHOD AND REAGENT FOR
TITLE OF INVENTION: TREATMENT OF PIRIOSIS AND
TITLE OF INVENTION: PIRIOSIS TREATMENT
NUMBER OF SEQUENCES: 67
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 611 West Sixth Street

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 1070000015-44
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/733,109
 FILING DATE: 25 OCTOBER 1996
 APPLICATION NUMBER: 08/870,910
 FILING DATE: 6 JUNE 1997
 APPLICATION NUMBER: 08/897,351
 FILING DATE: 21 JULY 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR DESCRIPTION:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' fluoro (U' F)
 FEATURE:
 OTHER INFORMATION: Features are 2' deoxy (U' U) modified
 FEATURE:
 OTHER INFORMATION: A 12 base GC rich region is a
 unmodified (U' U) 2' OH
 SEQUENCE DESCRIPTION: SEQ ID NO: 81:
 US-09-254-968-51
 Query Match 46.0% Score 13.9 DB 4 Length 29
 Best Local Similarity 22.0% Field No. 11e+03
 Matches 12, Conservative 3, Mismatches 2, Indels 0, Gaps 0
 CY 6 TCGCGAGAGAGATG 22
 C 6 TCGCGAGAGAGATG 22
 DB 6 TCGCGAGAGAGATG 22
 RESULT 23
 US-08-870-930-53
 Sequence 55, Application US/08870930
 Patent No. 6168778
 GENERAL INFORMATION:
 APPLICANT: NERGENA LIMITED, LARRY JELD, FRED J. JENSEN, CHARLSEA VANDERBEEK, MICHAEL
 TITLE OF INVENTION: VACCINAR ENDOGENIC GROWTH FACTOR VECTORS
 TITLE OF INVENTION: NUTRITIVE AGENT LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschuh, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/870,930
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: C12
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR DESCRIPTION:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' fluoro
 FEATURE:
 OTHER INFORMATION: Features are 2' deoxy (U' U) modified
 FEATURE:
 OTHER INFORMATION: A 12 base GC rich region is a
 unmodified (U' U) 2' OH
 SEQUENCE DESCRIPTION: SEQ ID NO: 81:
 US-09-254-968-51

TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR DESCRIPTION:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' fluoro
 FEATURE:
 OTHER INFORMATION: Features are 2' deoxy (U' U) modified
 FEATURE:
 OTHER INFORMATION: A 12 base GC rich region is a
 unmodified (U' U) 2' OH
 SEQUENCE DESCRIPTION: SEQ ID NO: 81:
 US-09-254-968-51
 Query Match 46.0% Score 13.9 DB 4 Length 30
 Best Local Similarity 22.0% Field No. 11e+03
 Matches 12, Conservative 3, Mismatches 2, Indels 0, Gaps 0
 CY 6 TCGCGAGAGAGATG 22
 C 6 TCGCGAGAGAGATG 22
 DB 6 TCGCGAGAGAGATG 22
 RESULT 24
 US-09-254-968-59
 Sequence 59, Application US/09254968
 Patent No. 6426335
 GENERAL INFORMATION:
 APPLICANT: NERGENA LIMITED, LARRY JELD, FRED J. JENSEN, CHARLSEA VANDERBEEK, MICHAEL
 TITLE OF INVENTION: VACCINAR ENDOGENIC GROWTH FACTOR VECTORS
 TITLE OF INVENTION: ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschuh, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/09254,968
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: C12
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR DESCRIPTION:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 30
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/254,968
 FILING DATE: 13-Mar-2000
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US/97/19944
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/033,103
 FILING DATE: 06 JUN 1997
 APPLICATION NUMBER: 08/097,351
 FILING DATE: 21 JULY 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: NEXT/CT/ECT-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ. 15 NO. 73:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
 modified
 FEATURE:
 OTHER INFORMATION: Induced and 2'-Methyl (2'-OMe) modified
 FEATURE:
 OTHER INFORMATION: G in position 10 and A in position 12 are
 unmodified (1.e., 2'-OH)
 SEQUENCE CHARACTERISTICS: SEQ. 16 NO. 74:
 US-09-254-968-75
 Query Match 46.0% Score 13.81 DR 4 Length 29
 Best Local Similarity 70.6% Prod. No. 11e+03
 Matches 12 Conservative 3 Mismatches 2 Indels 0 Gaps 0

27 6 TGGGAGAGAGAAATTG 22
 ||||| ||||| |||||
 28 6 UUCGAGAGAGAAAUUG 22

RESULT 21
 US-09-254-968-80
 Sequence 80, Application US/09254968
 Patent No. 6426335
 GENERAL INFORMATION:
 APPLICANT: MICHAEL WILLIS
 TITLE OF INVENTION: VACCINAR ENDOPEPTIDAL PEPTIDE ESTER (VEEP) COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Kratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/254,968
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: Unknown

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/254,968
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: Unknown
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCT/US/97/19944
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/033,109
 FILING DATE: 25 OCTOBER 1996
 APPLICATION NUMBER: 08/030,930
 FILING DATE: 6 JUNE 1997
 APPLICATION NUMBER: 08/097,351
 FILING DATE: 21 JULY 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DOCKET NUMBER: NEXT/CT/ECT-US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ. 15 NO. 80:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
 modified
 FEATURE:
 OTHER INFORMATION: Purines are 2'-O-methyl (2'-OMe) modified
 FEATURE:
 OTHER INFORMATION: G in positions 10 and 22 are unmodified
 (1.e., 2'-OH)
 SEQUENCE CHARACTERISTICS: SEQ. 16 NO. 81:
 US-09-254-968-80
 Query Match 46.0% Score 13.81 DR 4 Length 29
 Best Local Similarity 70.6% Prod. No. 11e+03
 Matches 12 Conservative 3 Mismatches 2 Indels 0 Gaps 0

27 6 TGGGAGAGAGAAATTG 22
 ||||| ||||| |||||
 28 6 UUCGAGAGAGAAAUUG 22

RESULT 22
 US-09-254-968-81
 Sequence 81, Application US/09254968
 Patent No. 6426335
 GENERAL INFORMATION:
 APPLICANT: MICHAEL WILLIS
 TITLE OF INVENTION: VACCINAR ENDOPEPTIDAL PEPTIDE ESTER (VEEP) COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Kratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/254,968
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: Unknown

RESULT 18
 US 09-870-930-77
 Sequence 77 Application US/0404090
 Patent No. 616078
 GENERAL INFORMATION:
 APPLICANT: HERCOSA VENTURE, LARRY GOLD, PAUL J. SCHMITZ, CHANDEA VANDERBEE, MICHAEL
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INHIBITORS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INHIBITORS
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESS: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Wulfsberg 9.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/070,930
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,113
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3411
 INFORMATION FOR SEQ ID NO. 77:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' modified
 FEATURE:
 OTHER INFORMATION: Positions are 2' modified (1-20)
 OTHER INFORMATION: modified
 FEATURE:
 OTHER INFORMATION: A in position 12 and 3
 OTHER INFORMATION: In position 12 and 3
 US 09-870-930-77
 Query Match: 46.0% Score 13.8, Pos 4, Length 29
 Best Local Similarity: 70.0%, Pos 1, Length 29
 Matches: 12, Conservative: 3, Mismatches: 2, Indels: 0, Gaps: 0
 CY 6 TGGCGAGGAGGATG 22
 DB 6 TGGCGAGGAGGATG 22
 RESULT 19
 US 09-254-968-79
 Sequence 79 Application US/0404090
 Patent No. 6426335
 GENERAL INFORMATION:
 APPLICANT: HERCOSA VENTURE, LARRY GOLD, PAUL J. SCHMITZ, CHANDEA VANDERBEE, MICHAEL
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INHIBITORS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INHIBITORS
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver

STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/254,968
 FILING DATE: 15 MAR 2000
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3411
 INFORMATION FOR SEQ ID NO. 78:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2' modified
 FEATURE:
 OTHER INFORMATION: Positions are 2' modified (1-20)
 OTHER INFORMATION: modified
 FEATURE:
 OTHER INFORMATION: A in position 12, and 3 in
 position 22 are unmodified (1-6, 2-20)
 US 09-254-968-79
 Query Match: 46.0% Score 13.8, Pos 4, Length 29
 Best Local Similarity: 70.0%, Pos 1, Length 29
 Matches: 12, Conservative: 3, Mismatches: 2, Indels: 0, Gaps: 0
 DB 6 TGGCGAGGAGGATG 22
 CY 6 TGGCGAGGAGGATG 22
 RESULT 20
 US 09-254-968-79
 Sequence 79 Application US/0404090
 Patent No. 6426335
 GENERAL INFORMATION:
 APPLICANT: HERCOSA VENTURE, LARRY GOLD, PAUL J. SCHMITZ, CHANDEA VANDERBEE, MICHAEL
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INHIBITORS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INHIBITORS
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:

REFERENCE/DECKET NUMBER: NEX61
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 14
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are
 OTHER INFORMATION: 2' fluoro (2'-F) modified
 FEATURE:
 OTHER INFORMATION: Purines are
 OTHER INFORMATION: 2'-O-methyl (2'-OMe) modified
 FEATURE:
 OTHER INFORMATION: G in position 10, A in position 12,
 OTHER INFORMATION: and G in position 22 are unmodified (1.00, 2'-OH)
 US-09-870-930-76

Query Match 46.0% Score 13.8; DB 4; Length 29;
 Best Local Similarity 70.6% Freq. No. 116+03;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0.
 CY 6 TGGGCGAGGAGGAAATG 22
 DB 6 TGGGCGAGGAGGAAATG 22

RESULT 16
 US-09-870-910-75
 Reference 75: Application US/9870930
 Patent No. 6168778
 GENERAL INFORMATION:
 APPLICANT: NEBOJSA JANTIC, LARRY GOLD, PAUL G. SCHMITZ, CHANINPA VAPRSESE, MICHAEL
 TITLE OF INVENTION: VASCULAR ENDOTHelial GROWTH FACTOR (VEGF)
 TITLE OF INVENTION: NUCLEIC ACID LIBRARY COMPLEXES
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Pratschuh, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/870,910
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DECKET NUMBER: NEX61
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 75:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro
 FEATURE:

OTHER INFORMATION: 1'-fluoro and 2'-O-methyl
 OTHER INFORMATION: (2'-OMe) modified
 FEATURE:
 OTHER INFORMATION: G in position 10 and A in
 OTHER INFORMATION: position 12 are unmodified (1.00, 2'-OH)
 US-09-870-930-75

Query Match 46.0% Score 13.8; DB 4; Length 29;
 Best Local Similarity 70.6% Freq. No. 116+03;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0.
 CY 6 TGGGCGAGGAGGAAATG 22
 DB 6 TGGGCGAGGAGGAAATG 22

RESULT 17
 US-09-870-930-76
 Reference 76: Application US/09870930
 Patent No. 6168778

GENERAL INFORMATION:
 APPLICANT: NEBOJSA JANTIC, LARRY GOLD, PAUL G. SCHMITZ, CHANINPA VAPRSESE, MICHAEL
 TITLE OF INVENTION: VASCULAR ENDOTHelial GROWTH FACTOR (VEGF)
 TITLE OF INVENTION: NUCLEIC ACID LIBRARY COMPLEXES
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Pratschuh, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 8.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/870,930
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/DECKET NUMBER: NEX61

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 76:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA

FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro
 FEATURE:
 OTHER INFORMATION: Purines are 2'-O-methyl
 FEATURE:
 OTHER INFORMATION: G in position 10 and A in
 OTHER INFORMATION: position 12 are unmodified (1.00, 2'-OH)
 US-09-870-930-76

Query Match 46.0% Score 13.8; DB 4; Length 29;
 Best Local Similarity 70.6% Freq. No. 116+03;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0.

CY 6 TGGGCGAGGAGGAAATG 22
 DB 6 TGGGCGAGGAGGAAATG 22

STREET: 8400 East Frontview Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
(C) OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/09/1994, 96d
FILING DATE: 13 Mar 2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/09/1994
FILING DATE: 17 OCTOBER 1997
APPLICATION NUMBER: 09/09/1996
FILING DATE: 25 OCTOBER 1996
APPLICATION NUMBER: 09/09/1996
FILING DATE: 6 JUNE 1997
APPLICATION NUMBER: 09/09/1997
FILING DATE: 21 JULY 1997

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/AGENT NUMBER: 17-101 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
modified

SEQUENCE DESCRIPTION: SEQ ID NO: 60:
US-09-254-968-60

Query Match: 46.0% Score 13.9; DB 4; Length 28;
Best Local Similarity 70.6% Pred. No. 1,1e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 5 TGGCGAGAGAGATG 22
DB 6 UGGGAGAGAGAGAG 22

RESULT 14
US-09-254-968-61
Sequence 7: Alignment: 09/09/1994
Patent No. 6168778
GENERAL INFORMATION:
APPLICANT: HERBERT CANTO, JEFFREY J. FAY, J. SCHWARTZ, CHANDEA VARGHESE,
MICHAEL WILLIS
ADDRESSER: Swanson and Patschold, L.L.C.
STREET: 8400 East Frontview Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
(C) OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/09/1994, 96e
FILING DATE: 13 Mar 2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/09/1994
FILING DATE: 17 OCTOBER 1997
APPLICATION NUMBER: 09/09/1996
FILING DATE: 25 OCTOBER 1996
APPLICATION NUMBER: 09/09/1996
FILING DATE: 6 JUNE 1997
APPLICATION NUMBER: 09/09/1997
FILING DATE: 21 JULY 1997

ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/AGENT NUMBER: 17-101 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433

INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
modified

SEQUENCE DESCRIPTION: SEQ ID NO: 61:
US-09-254-968-61

Query Match: 46.0% Score 13.9; DB 4; Length 28;
Best Local Similarity 70.6% Pred. No. 1,1e+03;
Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 5 TGGCGAGAGAGATG 22
DB 5 UGGGAGAGAGAGAG 21

RESULT 15
US-08-870-930-74
Sequence 7: Alignment: 09/09/1994
Patent No. 6168778
GENERAL INFORMATION:
APPLICANT: HERBERT CANTO, JEFFREY J. FAY, J. SCHWARTZ, CHANDEA VARGHESE, MICHAEL WILLIS
ADDRESSER: Swanson and Patschold, L.L.C.
STREET: 8400 East Frontview Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 8.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: 09/09/1994
FILING DATE: 6 JUNE 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215

Patent No. 611067
 GENERAL INFORMATION:
 APPLICANT: KING, HOLMIR
 APPLICANT: HIGGINS, LAUREN S.
 APPLICANT: TALION, MICHAEL
 APPLICANT: KUGERA, REBECCA B.
 APPLICANT: SCHILDKRAUT, IRA
 TITLE OF INVENTION: Cloning and Producing The N-Batch Nicking Endonuclease
 FILE REFERENCE: NEB 178
 CURRENT APPLICATION NUMBER: US09/0907030
 CURRENT FILING DATE: 2000-06-02
 NUMBER OF SEQ. NO. 27
 SOFTWARE: Patent In Ver. 2.0
 SEQ. NO. 17
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Bacillus stearothermophilus
 US 09-586-935-17

Query Match 46.08; Score 14; DB 4; Length 25;
 Best Local Similarity 77.38; Freq. No. 8,326,02;
 Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CY 6 TGGGAGAGAGAAATTTCT 2/
 24 TGGGAGAGAGAAATTTCT 3

RESULT 11
 US 08-870-930-56

Sequence 56; Application US/08/0930
 Patent No. 6168778

GENERAL INFORMATION:
 APPLICANT: NEROGA JANIS, LARRY GOLD, PAUL G. SCHMITT, CHARLEA VARGENSE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

NUMBER OF SEQUENCES: 24

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 4400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: WordPerfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US08/0907030

FILING DATE: 6 JUNE 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/COCKET NUMBER: NEXI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ. NO. 56:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2' deoxy

US 08-870-930-56

Query Match 46.08; Score 14; DB 4; Length 25;
 Best Local Similarity 70.61; Freq. No. 1,126,01;

Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

CY 6 TGGGAGAGAGAAATTTCT 2/
 24 TGGGAGAGAGAAATTTCT 3

RESULT 12
 US-08-870-930-57

Sequence 57; Application US/08/0907030
 Patent No. 6168778

GENERAL INFORMATION:

APPLICANT: NEROGA JANIS, LARRY GOLD, PAUL G. SCHMITT, CHARLEA VARGENSE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 4400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: WordPerfect 8.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/870,930

FILING DATE: 6 JUNE 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/COCKET NUMBER: NEXI

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

INFORMATION FOR SEQ. NO. 57:

SEQUENCE CHARACTERISTICS:

LENGTH: 28

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2' deoxy

US-08-870-930-57

Query Match 46.08; Score 13.8; DB 4; Length 28;
 Best Local Similarity 70.61; Freq. No. 1,126,01;
 Matches 12; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

RESULT 13
 US-09-254-968-60

Sequence 60; Application US/09/254968
 Patent No. 6426335

GENERAL INFORMATION:

APPLICANT: NEROGA JANIS, LARRY GOLD, PAUL G. SCHMITT, CHARLEA VARGENSE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

NUMBER OF SEQUENCES: 139

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.

NAME: CHARLES A. MOSERLIAN
 REGISTRATION NUMBER: 19,693
 REFERENCE/DOCKET NUMBER: 146,1159
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-661-8000
 TELEFAX: 212-661-8002
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24
 TYPE: NUCLEOTIDE
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: Oligonucleotide
 FEATURE:
 NAME/KEY:
 OTHER INFORMATION: TYPE Y ALPHA 15
 US-09-437-952A-75

Query Match 46.7% Score 14, E-01, Length 24,
 Best Local Similarity 77.8%, Seed No. 8,260,02,
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

QY 7 GGGGACAGGAGATTTCTG 28
 |||||||
 DB 22 GGTGACAGTGAATGCTG 1

RESULT 9
 US-09-459-205-4670
 Sequence 46, Application US/08559205
 Patent No. 6,247,012
 GENERAL INFORMATION:
 APPLICANT: Dau, Peter C.
 TITLE OF INVENTION: Method of identifying flanking regions of the 5' end of a nucleic acid
 NUMBER OF SEQUENCES: 61
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MARSHALL, CITICORP, BANKING, 100 WALL STREET, 6TH FLOOR, NEW YORK, NY 10038
 CITY: CHICAGO
 STATE: ILLINOIS
 COUNTRY: United States of America
 ZIP: 60606-6403
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patented Release #102, Version #1.03
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/459,205
 CLASSIFICATION: 436
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Gase, David A.
 REGISTRATION NUMBER: 38,103
 REFERENCE/DOCKET NUMBER: 18,011/00702
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 312/471-6700
 TELEFAX: 312/471-6448
 TELEX: 25-3856
 INFORMATION FOR SEQ ID NO: 46:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA
 US-09-559-205-46

Query Match 46.7% Score 14, E-01, Length 24,
 Best Local Similarity 77.8%, Seed No. 8,260,02,
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

QY 7 GGGGACAGGAGATTTCTG 28
 |||||||
 DB 22 GGTGACAGTGAATGCTG 1

RESULT 9
 US-09-041-0908-4370
 Sequence 43, Application US/090410908
 Patent No. 6,145,516
 GENERAL INFORMATION:
 APPLICANT: HERBERT, THIBERT, HILBBY, FREDERIC
 TITLE OF INVENTION: METHOD OF IDENTIFYING SEQUENCES OF THE 5' END OF A NUCLEIC ACID
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERNAN & MOSERLIAN
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/041,0908
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. MOSERLIAN
 REGISTRATION NUMBER: 19,693
 REFERENCE/DOCKET NUMBER: 146,1159
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-661-8002
 TELEFAX: 212-661-8000
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24
 TYPE: NUCLEOTIDE
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: Oligonucleotide
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: TYPE Y ALPHA 15, CLONE AB21, POSITION
 OTHER INFORMATION: 114
 US-09-041-0908-43

Query Match 46.7% Score 14, E-01, Length 24,
 Best Local Similarity 77.8%, Seed No. 8,260,02,
 Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0,

QY 7 GGGGACAGGAGATTTCTG 28
 |||||||
 DB 22 GGTGACAGTGAATGCTG 1

RESULT 10
 US-09-041-0908-4370
 Sequence 43, Application US/090410908
 Patent No. 6,145,516
 GENERAL INFORMATION:
 APPLICANT: HERBERT, THIBERT, HILBBY, FREDERIC
 TITLE OF INVENTION: METHOD OF IDENTIFYING SEQUENCES OF THE 5' END OF A NUCLEIC ACID
 NUMBER OF SEQUENCES: 62
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: BERNAN & MOSERLIAN
 CITY: NEW YORK
 STATE: NEW YORK
 COUNTRY: USA
 ZIP: 10016
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY DISK
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: WORDPERFECT 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/041,0908
 FILING DATE:
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:
 NAME: CHARLES A. MOSERLIAN
 REGISTRATION NUMBER: 19,693
 REFERENCE/DOCKET NUMBER: 146,1159
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-661-8002
 TELEFAX: 212-661-8000
 INFORMATION FOR SEQ ID NO: 43:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24
 TYPE: NUCLEOTIDE
 STRANDEDNESS: SINGLE
 TOPOLOGY: LINEAR
 MOLECULE TYPE: Oligonucleotide
 FEATURE:
 NAME/KEY:
 LOCATION:
 IDENTIFICATION METHOD:
 OTHER INFORMATION: TYPE Y ALPHA 15, CLONE AB21, POSITION
 OTHER INFORMATION: 114
 US-09-041-0908-43

APPLICANT: Strader, C.D.
TITLE OF INVENTION: Human Nucleotide Sequences
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSER: Merck & Co., Inc.
STREET: P.O. Box 2000
CITY: Rahway
STATE: New Jersey
COUNTRY: USA
ZIP: 07065-0807
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.05
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/483,371
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,168
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Thico, J.E.
REGISTRATION NUMBER: P-35,382
REFERENCE/OTHER NUMBER: 1998
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3904
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 33 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-09 483 371-15
Query March 59.0% Score 16, Gap 4, Length 33,
Best Local Similarity 78.3% Pred. No. 3, 1e+02;
Matches 18, Conservative 0, Mismatches 5, Indels 0, Gaps 0;
CY 3 MATCGCGTACGAGAGATGCTT 25
DB 1 MATTCGGCGGAGAGAGATGCT 23
RESULT 4
US-09-483-371 25/2
Sequence 42, Application US/08412283
Patent No. 6700909
GENERAL INFORMATION:
APPLICANT: HERGENO, THIRRY, TRIBEL, FERRELL
APPLICANT: FOMAN-ROMAN, SERGIO, FERRADINI, LAURENT
TITLE OF INVENTION: NOVELTY-TESTING OF HUMAN T
TITLE OF INVENTION: VARIABLE REGION OF HUMAN T
TITLE OF INVENTION: REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION AND THE
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRMAN & MUSELLAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/483,371

FILING DATE: 14 APR-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/934,510
FILING DATE: 23 NOV 1992
APPLICATION NUMBER: US/832/00130
FILING DATE: 12 FEB 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR/91/01613
FILING DATE: 12-FEB-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR/91/034703
FILING DATE: 12-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: CHARLES A. MUSELLAN
REGISTRATION NUMBER: 10,083
REFERENCE/OTHER NUMBER: 446,1108
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-661-8002
TELEFAX: 212-661-8002
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 24
TYPE: NUCLEOTIDE
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: OLIGONUCLEOTIDE
FEATURE:
NAME/KEY:
OTHER INFORMATION: TYPE V Alpha 18
US-09-423-393 75
Query March 46.7% Score 14, DB 1, Length 24,
Best Local Similarity 77.3% Pred. No. 8, 2e+02;
Matches 17, Conservative 0, Mismatches 5, Indels 0, Gaps 0;
CY 7 GCGGACGAGAGAGATGCTG 28
DB 22 GTTCAGCGAGATGCTG 1
RESULT 5
US-09-620-467A-42/C
Sequence 42, Application US/08620467A
Patent No. 5798231
GENERAL INFORMATION:
APPLICANT: HERGENO, THIRRY, TRIBEL,
APPLICANT: FOMAN-ROMAN, SERGIO, FERRADINI,
APPLICANT: LAURENT
TITLE OF INVENTION: NOVELTY-TESTING OF HUMAN T
TITLE OF INVENTION: VARIABLE REGION OF THE CHAIN OF HUMAN T
TITLE OF INVENTION: REVERSE TRANSCRIPTION POLYMERASE CHAIN REACTION, CORRESPONDING FERTILE
TITLE OF INVENTION: ALLELES AND DIAGNOSTIC AND THERAPEUTIC USES
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSER: BIRMAN & MUSELLAN
STREET: 600 THIRD AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: USA
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/620,467A
FILING DATE: 22 MAR 1996
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/348,072

[illegible]

XX Example 4: Page 93: 128pb: English.

PS Sequences were determined from the ends of chromosome 11-specific

CC sequenced by integrated sequencing without intermediate subcloning.

CC A total of 121 DNA sequences fragments were determined and of

CC these, 277 were suitable for STS primer prediction by computer.

CC analysis using the "Primer" program available from E. Landier, MIT).

CC The results of this analysis were affected by in situ hybridization, serial

CC cell hybrid analysis or both using this method, 370 STS specific

CC for human chromosome 11 were generated and most of them were

CC regionally mapped. This procedure illustrates a novel method for

CC sequencing complex genomes. Assigned "regionally mapped" method for

CC The sequence sampled mapping method is useful for the completion of

CC high density sequence-based maps, and ultimately, for the complete

CC sequencing of genomic DNA directly from cosmid clones.

CC See AAG49474 (28/70) and AAG49475 (28/70) for STS primers.

CC

XX

50 Sequence to bp: 9 A: 10 G: 6 G: 5 T: 0 other:

Query Match 50.0% Score 157 DB 16: Length 307

Post Local Similarity 79.3% Pred No: 4.8e+03

Matches 18: Conservative 0: Mismatches 5: Indels 0: Gaps 0

6 TGGCGGAGGAGGAGTGTCTG 28

|||||

28 TGGCGGAGGAGGAGTGTCTG 6

RESULT 18

AA049474

18 AA049474 standard: DNA: 33 BP.

XX

AC AA049474:

XX

DT 14-APR-1994 (first entry)

XX

DE Primer "4832" to amplify human NTRP N (terminal) -1000

XX

XX human, "neurokinin receptor" (NTRP) (clonally: neurokinin B

KW tachykinin encephalin release) ss.

XX

OS Synthetic.

XX

PN GR2265375 A.

XX

PD 29-SEP-1993.

XX

PF 06-MAR-1993: 9306 0004/04

XX

PR 16-MAR-1992: 9203 0851/974.

XX

PA (MERT) MERCK & CO INC

XX

PI Fong TM, Huang RRC, Strader CD:

XX

XX WPI: 133-305637/33.

XX

PT How regionally mapped human NTRP N (terminal) -1000 to identify

XX

XX binding ligands, antagonists and agonists of the receptor

XX

XX Example 1: Page 18: 471b: English.

CC Dependent on the effects were designed based on the known sequence of

CC rat NTRP (rat neurokinin receptor). The corresponding human cDNA

CC sequence was 4.1 kb by amplification of human brain cDNA. Two

CC primers corresponding to the human sequence were designed and anchored

CC PCR was performed using the human primer in the core region.

CC To isolate a clone coding for the N-terminal region of human NTRP,

CC cDNA synthesis was initiated with primers "AAG49471" and

CC "A400" (AA049473) and then a polyA tail was added. A library PCR was

CC carried out using primers "AAG49471" and "A400" (AA049473) and

CC "A400" (AA049473) and "A400" (AA049473) and "A400" (AA049473) with

CC "A400" (AA049473) and a 60bp cDNA fragment which encodes the

CC N-terminal region of human NTRP and the 5'-UTR was obtained and

CC sequenced. The c-terminal coding region was similarly obtained.

CC Finally a full-length cDNA (AA049473) was obtained in a single step

CC using primers from the 5' and 3' untranslated regions. The human

CC NTRP sequence with the useful for food (103: 00) and proteins and

CC antagonists.

XX

50 Sequence to bp: 9 A: 6 G: 10 T: 0 other:

Query Match 50.0% Score 157 DB 16: Length 307

Post Local Similarity 79.3% Pred No: 4.8e+03

Matches 18: Conservative 0: Mismatches 5: Indels 0: Gaps 0

3 AATTCGCGGAGGAGGAGTGTCTG 28

|||||

1 AATTCGCGGAGGAGGAGTGTCTG 23

RESULT 19

AA078196/C

19 AA078196 standard: DNA: 32 BP.

XX

AC AA078196:

XX

DT 28-JUL-1995 (first entry)

XX

DE Primer to amplify cDNA to obtain DNA-4 for construction of pTA100

XX

XX VIP: vasopressin intestinal polypeptide; analogues, leader peptide

KW Sarcophaga (fused) fused proteins, vasodilators, hypotensive activity

KW smooth muscle relaxant, intestinal juice secretion suppressant, ss.

XX

OS Synthetic.

XX

PN EF622459-A.

XX

PD 02-NOV-1994.

XX

PF 25-APR-1994: 9450 0100/92.

XX

PR 26-APR-1993: 9330 0009/13.

XX

PA (SANWA) SANWA KAGAKU KENYUSHO CO.

XX

PI Hirade K, Kobayashi Y, Mitani T, Nishida M, Sakai K

XX

PI Takahashi H:

XX

DP WPI: 1994-334644/42.

XX

PT Fused proteins used for preparing vasopressin analogues

XX

PT polypeptide analogues in large quantities and which have

XX

PT potent biological activity

XX

XX Example 1: Page 9: 42pb: English.

CC Primers AA078196 7 were used to amplify a cDNA clone described in

CC Pict. Chem Vol 20, pp 1029-13 (1995). The PCR product was treated

CC with EcoRI and HindIII to obtain two 4 kb fragments. The PCR

CC product was then ligated to pTA100 to obtain pTA100.

CC pTA100 is useful for the expression of Sarcophaga leader peptide

CC (the production of a fused protein with VIP leader peptide) and

CC polypeptide analogues, which comprises a leader peptide (LP) derived

CC from Sarcophaga leader peptide and at least one molecule arranged in tandem of this

CC sequence. This peptide is linked to the LP to stabilize the fused protein

CC as an insecticide body.

XX

50 Sequence to bp: 9 A: 6 G: 10 T: 0 other:

Query Match 49.7% Score 1457 DB 16: Length 327

Post Local Similarity 79.3% Pred No: 4.8e+03

Matches 17: Conservative 0: Mismatches 4: Indels 0: Gaps 0

Query Match 51.3% Score 15.4; DB 24; Length 35;
 Best Local Similarity 76.0%; Pred. No. 33e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Cy 5 TTGTCGACAGAGAAATTTTCCT 29
 |||||
 Db 3 TGGGCGCGCGAGAAATTTTTCCT 27

RESULT 11
 ABR71510
 29 ABR71510 standard; DNA; 35 BP.
 AC ABR71510;
 DE 30-JUL-2002 (first entry)
 DE CNS related 3' sequencing primer:
 XX Central nervous system; CNS; neuroleptic; mouse; human; psychoses;
 XX neuropsychiatric disorder; psychiatric disorder; Alzheimer's disease;
 XX Pick's disease; Pickman's disease; senile dementia; senile dementia;
 XX Parkinson's disease; obsessive-compulsive disorder; epilepsy;
 XX schizophrenia; addiction; multiple sclerosis; depression;
 XX manic-depressive disorder; primer; ss.
 XX Synthetic:
 XX WGCAGG226936 A2.
 XX 04-APR-2002.
 XX 01-OCT-2001; 2001W0-0530025.
 XX 29-SEP-2000; 2000US-2467992.
 XX 18-JAN-2001; 2001US-263984P.
 XX (DIGIT-) DIGITAL GENE TECHNOLOGIES INC.
 XX Thomas EA, Sutcliffe JG, Pribyl TM, Hirsch ES, Harel KM;
 DE WPI; 2002-183271/41.
 XX New polynucleotide useful in gene therapy for preventing, treating
 PT modulating or activating a cell or a cell line, such as lymphocytes in a
 PT neuro-psychiatric disorder or a schizophrenia, or a bipolar disorder in
 PT a mammal.
 XX Example 1; page 232, 254pp, English.

CC This invention relates to the CNS sequences of novel isolated
 CC polynucleotide sequences with psychoses or other neurodegenerative
 CC disorders. The sequences of the invention may act as receptors of D
 CC receptors in the central nervous system. The sequences of the invention
 CC of the invention and the polypeptides encoded by them are useful in the
 CC manufacturing of a medicament useful for preventing, treating, or
 CC ameliorating a medical condition or a neuro-psychiatric disorder.
 CC antibody that binds the protein of the invention is useful for
 CC preventing, treating, modulating or activating neuro-psychiatric
 CC such as psychoses or other neuro-psychiatric disorders in a mammal. The
 CC sequences are also useful for diagnosing neuro-psychiatric disorders.
 CC susceptibility to a neuro-psychiatric disorder such as psychoses and other
 CC neuro-psychiatric disorders in a subject by determining the presence or
 CC absence of mutation in the nucleotide sequence of apolipoprotein B or by
 CC determining the alteration (insertion, deletion) in the expression of
 CC apolipoprotein B. The sequences of the invention are useful in treating
 CC deficiencies or disorders of the central nervous system or peripheral
 CC nervous system by activating or inhibiting the protein of the
 CC differentiation or cell growth of neuro-psychiatric disorders such as
 CC or glial cells. The sequences are useful as a marker of the onset of a
 CC particular neuro-psychiatric disorder such as Alzheimer's disease,
 CC Pick's disease, Pickman's disease, senile dementia, senile dementia,
 CC Parkinson's disease, obsessive-compulsive disorder, epilepsy,
 CC schizophrenia, addiction, multiple sclerosis, depression,

CC schizophrenia; ischemia; addiction; multiple sclerosis; depression;
 CC Alzheimer's disease; Alzheimer's disease; the present sequence represents an
 CC polynucleotide primer used in the identification of the above disorders
 CC of the invention.

SQ Sequence 35 BP; 3 A; 4 G; 9 T; 0 other;

Query Match 51.3% Score 15.4; DB 24; Length 35;
 Best Local Similarity 76.0%; Pred. No. 33e+03;
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Cy 5 TTGTCGACAGAGAAATTTTCCT 29
 |||||
 Db 3 TGGGCGCGCGAGAAATTTTTCCT 27

RESULT 12
 AAD34664
 ID AAD34664 standard; DNA; 35 BP.
 AC AAD34664;
 DE 16-JUN-2002 (first entry)
 DE PCR primer #5 used for direct sequencing of TOGA generated POP products.
 XX Hepatitis B virus; HBV infection; chronic hepatitis; toxicity; virology;
 XX acute hepatitis; therapeutic; gene therapy; vaccine; infectious diseases;
 XX (TOGA) Total Gene Expression Analysis (TGA) primer; ss.
 XX Unidentified.
 XX WGCAGG22783 A2.
 XX 21-MAR-2002.
 XX 11-SEP-2001; 2001W0-0530123.
 XX 15-SEP-2000; 2000US-233176P.
 XX (DIGIT-) DIGITAL GENE TECHNOLOGIES INC.
 XX Chisari FV, Wieland SF, Guidotti LGVM, Mueller F, Hirsch ES;
 DE WPI; 2002-339850/37.
 XX Preventing and treating hepatitis viral infection in a mammal,
 PT comprising administering nucleic acid molecules that up- or
 PT down-regulate in hepatitis B virus infected cells polypeptide encoded by
 PT the nucleic acid molecules.
 XX Example 1; page 25, 26pp, English.

CC The present invention relates to a method for preventing, treating,
 CC modulating or ameliorating a medical condition. The method involves
 CC administering to a subject a polynucleotide sequence of a down-regulated
 CC polypeptide or a polypeptide encoded by the polynucleotide. The
 CC nucleic acid molecules or nucleotides that bind to the polypeptide. The
 CC method is useful for preventing, treating, modulating or activating
 CC a medical condition. It is also useful for determining the presence or
 CC absence of a mutation in the nucleic acid molecule or detecting an
 CC alteration in the expression of the polypeptide which is useful for the
 CC diagnosis of hepatitis viral infection. The method is useful for
 CC assessing the stage of hepatitis viral infection (e.g., acute hepatitis
 CC versus chronic hepatitis) or assessing the efficacy of a therapy of
 CC therapeutic treatment for hepatitis viral infection and a gene expression
 CC profile is useful for identifying polypeptides and polynucleotides which
 CC are associated with hepatitis viral infection. Sequences of the invention
 CC are used in gene therapy and as vaccines. Nucleic acid sequences are
 CC useful as a diagnostic marker for HBV infection and for treating
 CC hepatitis B virus. The present invention also provides a method which
 CC is used for direct sequencing of total gene expression analysis
 CC generated for products.

PT polymerside to ceramxin protein
 XX
 PS Example 1: Page 17: 64PP: English
 XX
 CC This invention describes a novel formulation (1) for use in therapeutic
 CC and/or cosmetic treatment of a skin condition, or an anti-aging
 CC formulation, which is a ceramxin protein complexed with a carrier or
 CC vehicle. The primary of the invention have been: (i) a carrier, (ii)
 CC an inflammatory and dermatological activity, (iii) is useful in a
 CC formulation (1) which is administered to a site on or within a patient
 CC for the site-specific downregulation of ceramxin protein expression. (1)
 CC is therefore specifically useful for reducing neuronal cell death
 CC resulting from neuronal insult to a specific site in the brain, spinal
 CC cord or peripheral nerve of a patient, for promoting wound healing resulting
 CC from trauma, burns or surgery and for reducing inflammation as a result
 CC of a wound or physical trauma of the brain, spinal cord or peripheral
 CC nerve and for dermal skin formation of a granular (1) directed to
 CC ceramxin at or in a skin condition to regulate epithelial basal cell
 CC division and growth or to regulate outer layer keratinization,
 CC respectively, for skin rejuvenation or thickening for cosmetic or
 CC therapeutic purposes (1) downregulates ceramxin expression in a highly
 CC desirable site-specific manner. This sequence represents a ceramxin-43
 CC directed (1) directed to which is used in the method of the invention.
 XX
 SQ Sequence 40 Ref: 7 A; 5 C; 9 G; 9 T; 0 other;
 Query Match 69.0%, Score 20.4, DB 21, Length 30,
 Pos: 12-41, Consistency 95.0%, Ident 88.3%,
 Matches 24; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 OY 1 GTATATGCGAGGAGGATTTCTCTC 30
 1 GTATATGCGAGGAGGATTTCTCTC 30
 1 GTATATGCGAGGAGGATTTCTCTC 30
 RESULT 5
 AAA09807
 ID AAA09807 standard; DNA; 20 BP.
 XX
 AC AAA09807;
 XX
 DT 24-MAR-1999 (first entry)
 XX
 DE Human biallelic polymorphic marker downstream primer #113.
 XX
 KW Polymorphism; biallelic; human; forensic; paternity testing; disease;
 KW polymorphism; polymorphic typing; characterization; infectious; hereditary;
 KW autoimmune disease; cancer; inflammation; drug; therapy; medication;
 KW forensic; marker; primer; ss
 XX
 OS Synthetic;
 OS Homo sapiens.
 XX
 PN W09820165 A2;
 XX
 PD 14 MAY 1998.
 XX
 PF 05-MAY-1998, 97MO GENE;
 XX
 PR 06-NOV-1996; 9605-0030455.
 XX
 PA (WHHD) WHITEHEAD INST BIOMEDICAL RES.
 XX
 FI Hudson T., Tardif F., Wang D.
 XX
 DR WPI: 1998 266974/75
 XX
 PT New isolated nucleic acid sequence from the human genome - used for
 PT determining polymorphic forms for use in a forensic; paternity
 PT testing or forensic typing for disease
 XX
 FT Title: Fig. 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 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1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 1835, 1836, 1837, 1838, 1839, 1840, 1841, 1842, 1843, 1844, 1845, 1846, 1847, 1848, 1849, 1850, 1851, 1852, 1853, 1854, 1855, 1856, 1857, 1858, 1859, 1860, 1861, 1862, 1863, 1864, 1865, 1866, 1867, 1868, 1869, 1870, 1871, 1872, 1873, 1874, 1875, 1876, 1877, 1878, 1879, 1880, 1881, 1882, 1883, 1884, 1885, 1886, 1887, 1888, 1889, 1890, 1891, 1892, 1893, 1894, 1895, 1896, 1897, 1898, 1899, 1900, 1901, 1902, 1903, 1904, 1905, 1906, 1907, 1908, 1909, 1910, 1911, 1912, 1913, 1914, 1915, 1916, 1917, 1918, 1919, 1920, 1921, 1922, 1923, 1924, 1925, 1926, 1927, 1928, 1929, 1930, 1931, 1932, 1933, 1934, 1935, 1936, 1937, 1938, 1939, 1940, 1941, 1942, 1943, 1944, 1945, 1946, 1947, 1948, 1949, 1950, 1951, 1952, 1953, 1954, 1955, 1956, 1957, 1958, 1959, 1960, 1961, 1962, 1963, 1964, 1965, 1966, 1967, 1968, 1969, 1970, 1971, 1972, 1973, 1974, 1975, 1976, 1977, 1978, 1979, 1980, 1981, 1982, 1983, 1984, 1985, 1986, 1987, 1988, 1989, 1990, 1991, 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 204

U00001	ADAMTS-1	1	100000000	100000000	+	Exon	U00001	ADAMTS-1	1	100000000	100000000	+	Exon
U00002	ADAMTS-2	2	200000000	200000000	+	Exon	U00002	ADAMTS-2	2	200000000	200000000	+	Exon
U00003	ADAMTS-3	3	300000000	300000000	+	Exon	U00003	ADAMTS-3	3	300000000	300000000	+	Exon
U00004	ADAMTS-4	4	400000000	400000000	+	Exon	U00004	ADAMTS-4	4	400000000	400000000	+	Exon
U00005	ADAMTS-5	5	500000000	500000000	+	Exon	U00005	ADAMTS-5	5	500000000	500000000	+	Exon
U00006	ADAMTS-6	6	600000000	600000000	+	Exon	U00006	ADAMTS-6	6	600000000	600000000	+	Exon
U00007	ADAMTS-7	7	700000000	700000000	+	Exon	U00007	ADAMTS-7	7	700000000	700000000	+	Exon
U00008	ADAMTS-8	8	800000000	800000000	+	Exon	U00008	ADAMTS-8	8	800000000	800000000	+	Exon
U00009	ADAMTS-9	9	900000000	900000000	+	Exon	U00009	ADAMTS-9	9	900000000	900000000	+	Exon
U00010	ADAMTS-10	10	1000000000	1000000000	+	Exon	U00010	ADAMTS-10	10	1000000000	1000000000	+	Exon
U00011	ADAMTS-11	11	1100000000	1100000000	+	Exon	U00011	ADAMTS-11	11	1100000000	1100000000	+	Exon
U00012	ADAMTS-12	12	1200000000	1200000000	+	Exon	U00012	ADAMTS-12	12	1200000000	1200000000	+	Exon
U00013	ADAMTS-13	13	1300000000	1300000000	+	Exon	U00013	ADAMTS-13	13	1300000000	1300000000	+	Exon
U00014	ADAMTS-14	14	1400000000	1400000000	+	Exon	U00014	ADAMTS-14	14	1400000000	1400000000	+	Exon
U00015	ADAMTS-15	15	1500000000	1500000000	+	Exon	U00015	ADAMTS-15	15	1500000000	1500000000	+	Exon
U00016	ADAMTS-16	16	1600000000	1600000000	+	Exon	U00016	ADAMTS-16	16	1600000000	1600000000	+	Exon
U00017	ADAMTS-17	17	1700000000	1700000000	+	Exon	U00017	ADAMTS-17	17	1700000000	1700000000	+	Exon
U00018	ADAMTS-18	18	1800000000	1800000000	+	Exon	U00018	ADAMTS-18	18	1800000000	1800000000	+	Exon
U00019	ADAMTS-19	19	1900000000	1900000000	+	Exon	U00019	ADAMTS-19	19	1900000000	1900000000	+	Exon
U00020	ADAMTS-20	20	2000000000	2000000000	+	Exon	U00020	ADAMTS-20	20	2000000000	2000000000	+	Exon
U00021	ADAMTS-21	21	2100000000	2100000000	+	Exon	U00021	ADAMTS-21	21	2100000000	2100000000	+	Exon
U00022	ADAMTS-22	22	2200000000	2200000000	+	Exon	U00022	ADAMTS-22	22	2200000000	2200000000	+	Exon
U00023	ADAMTS-23	23	2300000000	2300000000	+	Exon	U00023	ADAMTS-23	23	2300000000	2300000000	+	Exon
U00024	ADAMTS-24	24	2400000000	2400000000	+	Exon	U00024	ADAMTS-24	24	2400000000	2400000000	+	Exon
U00025	ADAMTS-25	25	2500000000	2500000000	+	Exon	U00025	ADAMTS-25	25	2500000000	2500000000	+	Exon

227	1.2	10.1	31	20	AA01587	PCR primer for human
228	1.2	40.0	32	24	AB01604	Human histone H1
229	1.2	10.1	33	24	AA01605	Primer used to amplify
230	1.2	40.0	34	24	AA01606	Primer used to amplify
231	1.2	10.1	35	24	AA01607	Primer used to amplify
232	1.2	40.0	36	24	AA01608	Primer used to amplify
233	1.2	40.0	37	24	AA01609	Primer used to amplify
234	1.2	40.0	38	24	AA01610	Primer used to amplify
235	1.2	40.0	39	24	AA01611	Primer used to amplify
236	1.2	40.0	40	24	AA01612	Primer used to amplify
237	1.2	40.0	41	24	AA01613	Primer used to amplify
238	1.2	40.0	42	24	AA01614	Primer used to amplify
239	1.2	40.0	43	24	AA01615	Primer used to amplify
240	1.2	40.0	44	24	AA01616	Primer used to amplify
241	1.2	40.0	45	24	AA01617	Primer used to amplify
242	1.2	40.0	46	24	AA01618	Primer used to amplify
243	1.2	40.0	47	24	AA01619	Primer used to amplify
244	1.2	40.0	48	24	AA01620	Primer used to amplify
245	1.2	40.0	49	24	AA01621	Primer used to amplify
246	1.2	40.0	50	24	AA01622	Primer used to amplify
247	1.2	40.0	51	24	AA01623	Primer used to amplify
248	1.2	40.0	52	24	AA01624	Primer used to amplify
249	1.2	40.0	53	24	AA01625	Primer used to amplify
250	1.2	40.0	54	24	AA01626	Primer used to amplify
251	1.2	40.0	55	24	AA01627	Primer used to amplify
252	1.2	40.0	56	24	AA01628	Primer used to amplify
253	1.2	40.0	57	24	AA01629	Primer used to amplify
254	1.2	40.0	58	24	AA01630	Primer used to amplify
255	1.2	40.0	59	24	AA01631	Primer used to amplify
256	1.2	40.0	60	24	AA01632	Primer used to amplify
257	1.2	40.0	61	24	AA01633	Primer used to amplify
258	1.2	40.0	62	24	AA01634	Primer used to amplify
259	1.2	40.0	63	24	AA01635	Primer used to amplify
260	1.2	40.0	64	24	AA01636	Primer used to amplify
261	1.2	40.0	65	24	AA01637	Primer used to amplify
262	1.2	40.0	66	24	AA01638	Primer used to amplify
263	1.2	40.0	67	24	AA01639	Primer used to amplify
264	1.2	40.0	68	24	AA01640	Primer used to amplify
265	1.2	40.0	69	24	AA01641	Primer used to amplify
266	1.2	40.0	70	24	AA01642	Primer used to amplify
267	1.2	40.0	71	24	AA01643	Primer used to amplify
268	1.2	40.0	72	24	AA01644	Primer used to amplify
269	1.2	40.0	73	24	AA01645	Primer used to amplify
270	1.2	40.0	74	24	AA01646	Primer used to amplify
271	1.2	40.0	75	24	AA01647	Primer used to amplify
272	1.2	40.0	76	24	AA01648	Primer used to amplify
273	1.2	40.0	77	24	AA01649	Primer used to amplify
274	1.2	40.0	78	24	AA01650	Primer used to amplify
275	1.2	40.0	79	24	AA01651	Primer used to amplify
276	1.2	40.0	80	24	AA01652	Primer used to amplify
277	1.2	40.0	81	24	AA01653	Primer used to amplify
278	1.2	40.0	82	24	AA01654	Primer used to amplify
279	1.2	40.0	83	24	AA01655	Primer used to amplify
280	1.2	40.0	84	24	AA01656	Primer used to amplify
281	1.2	40.0	85	24	AA01657	Primer used to amplify
282	1.2	40.0	86	24	AA01658	Primer used to amplify
283	1.2	40.0	87	24	AA01659	Primer used to amplify
284	1.2	40.0	88	24	AA01660	Primer used to amplify
285	1.2	40.0	89	24	AA01661	Primer used to amplify
286	1.2	40.0	90	24	AA01662	Primer used to amplify
287	1.2	40.0	91	24	AA01663	Primer used to amplify
288	1.2	40.0	92	24	AA01664	Primer used to amplify
289	1.2	40.0	93	24	AA01665	Primer used to amplify
290	1.2	40.0	94	24	AA01666	Primer used to amplify
291	1.2	40.0	95	24	AA01667	Primer used to amplify
292	1.2	40.0	96	24	AA01668	Primer used to amplify
293	1.2	40.0	97	24	AA01669	Primer used to amplify
294	1.2	40.0	98	24	AA01670	Primer used to amplify
295	1.2	40.0	99	24	AA01671	Primer used to amplify
296	1.2	40.0	100	24	AA01672	Primer used to amplify
297	1.2	40.0	101	24	AA01673	Primer used to amplify
298	1.2	40.0	102	24	AA01674	Primer used to amplify
299	1.2	40.0	103	24	AA01675	Primer used to amplify
300	1.2	40.0	104	24	AA01676	Primer used to amplify
301	1.2	40.0	105	24	AA01677	Primer used to amplify

[illegible]



Db 3 GGATTCAGAGCTGGAGATGTTCTC 28

RESULT 40
AX201854/c

LOCUS

30 bp

DNA

linear

FAT 30 AUG-2001

DEFINITION

Sequence 13 from Patent WO0153494.

ACCESSION

AX201854

VERSION

AX201854.1 GI:153494595

KEYWORDS

SOURCE

synthetic construct.

ORGANISM

synthetic construct.

REFERENCE

artificial sequences.

AUTHORS

1 (bases 1 to 30)

TITLE

Butler, A. and Carter, J. N.

Cloning and overexpression of a small, high-levelase from marine

algae

Patent: WO 0153494-A 13-26-01-2001

Journal

The Regents of the University of California (US)

FEATURES

Location/Qualifiers

1..30

source

/organism="synthetic construct"

/db_xref="taxon:32630"

/note="DNA"

BASE COUNT

8 a 8 c 5 g 9 t

ORIGIN

Query Match

44.0% Score 13.7, E-6, Length 30,

Best Local Similarity

93.3% Pos: No. 2, 3e+05,

Match: 15, Conservation: 0, Mismatch: 3, Indel: 0, Gaps: 0;

QY

2 TATTGCGGAGAGGAA 19

CH

18 TTATTGCTGAGAGGAA 1

Search completed: July 21, 2003, 14:34:49
CPU time: 321.497 secs

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REFERENCE 1 (bases 1 to 21)
AUTHORS   Palase, P. and Garcia-Sastre, A.
TITLE     Recombinant negative strand RNA viruses
JOURNAL   J. Virol. 73:1406-1411, 1999.
FEATURES   source
            /organism="unknown"

BASE COUNT      4 a      4 c      7 t

ORIGIN
Query Match      44.0% Score 13.2; DB 6; Length 21;
Best Local Similarity 83.3% Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 10 ATGACAAATTTCTTCT 20
    |||||
DB 2 AGGACAAATTTCTTCT 19

RESULT 36
AX394143/c
LOCUS      AX394143
DEFINITION Sequence 118 from Patient W00214966.
ACCESSION  AX394143
VERSION     AX394143.1 GI:19702093
KEYWORDS
SOURCE      synthetic construct.
            /organism="synthetic construct"
            /db_xref="taxon:12630"
            /note="sense primer C/CA4"
FEATURES
source
    1..25
    Location/Qualifiers
        /organism="synthetic construct"
        /db_xref="taxon:12630"
        /note="sense primer C/CA4"
BASE COUNT      7 a      7 c      5 g      6 t

ORIGIN
Query Match      44.0% Score 13.2; DB 6; Length 25;
Best Local Similarity 83.3% Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 8 GATCAGAGGAAATGTTT 25
    |||||
DB 21 GTTCAGAGGAAATGTTT 4

RESULT 37
AX44167/c
LOCUS      AX44167
DEFINITION Sequence 110 from Patient W00216599.
ACCESSION  AX44167
VERSION     AX44167.1 GI:19704044
KEYWORDS
SOURCE      synthetic construct.
            /organism="synthetic construct"
            /db_xref="taxon:12630"
            /note="sense primer C/CA4"
FEATURES
source
    1..27
    Location/Qualifiers
        /organism="synthetic construct"
        /db_xref="taxon:12630"
        /note="sense primer C/CA4"
BASE COUNT      10 a      10 c      10 g      7 t

ORIGIN
Query Match      44.0% Score 13.2; DB 6; Length 27;
Best Local Similarity 83.3% Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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BASE COUNT      5 a      8 c      4 g      10 t

ORIGIN
Query Match      44.0% Score 13.2; DB 6; Length 27;
Best Local Similarity 83.3% Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CY 6 TGGGTACGAGAAATGCT 23
    |||||
DB 24 TGGGTACGAGAAATGCT 7

RESULT 38
AX316347
LOCUS      AX316347
DEFINITION Sequence 35 from Patient W00190188.
ACCESSION  AX316347
VERSION     AX316347.1 GI:17899520
KEYWORDS
SOURCE      synthetic construct.
            /organism="synthetic construct"
            /db_xref="taxon:12630"
            /note="forward primer MBU-0 713; reverse primer"
FEATURES
source
    1..29
    Location/Qualifiers
        /organism="synthetic construct"
        /db_xref="taxon:12630"
        /note="forward primer MBU-0 713; reverse primer"
BASE COUNT      8 a      5 c      9 g      7 t

ORIGIN
Query Match      44.0% Score 13.2; DB 6; Length 29;
Best Local Similarity 83.3% Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

CY 1 GAAATGCGGAGAGAAATGTTT 29
    |||||
DB 3 GAAATGCGGAGAGAAATGTTT 28

RESULT 39
AX431255
LOCUS      AX431255
DEFINITION Sequence 19 from Patient W00240543.
ACCESSION  AX431255
VERSION     AX431255.1 GI:121556137
KEYWORDS
SOURCE      synthetic construct.
            /organism="synthetic construct"
            /db_xref="taxon:12630"
            /note="primer MBU-0 737"
FEATURES
source
    1..29
    Location/Qualifiers
        /organism="synthetic construct"
        /db_xref="taxon:12630"
        /note="primer MBU-0 737"
BASE COUNT      8 a      5 c      9 g      7 t

ORIGIN
Query Match      44.0% Score 13.2; DB 6; Length 29;
Best Local Similarity 83.3% Pred. No. 2.3e+05;
Matches 15; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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TITLE Vascular endothelial growth factor (VEGF) Nucleic Acid Ligand
 COMPLEXES
 PATENT: US 616979 A 55 02 JAN 2001;
 LOCATION/Qualifiers
 FEATURES
 SOURCE 1.30 /Organism="unknown"
 BASE COUNT 9 a 10 j 1 i
 ORIGIN

Query Match 46.0%; Score 13.8; DB 6; Length 30;
 Best Local Similarity 80.2%; Pred. No. 1 20075;
 Matches 17, Conservative 0, Mismatches 1, Indels 0, Dels 0

QY 6 TCGGAGAGAGATG 22
 |||||
 DP 6 TCGGAGAGAGATG 22

RESULT 31
 AR091236
 LOCUS AR091236 1106 bp. Exact 28 1000000
 DEFINITION AR091236
 ACCESSION AR091236
 VERSION AR091236.1 GI:10017991
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Chenchik, A., Jekhadze, G. and Bihlachevillir, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 590476-A 1999 30-NOV-1999;
 FEATURES
 SOURCE Location/Qualifiers
 1..28

BASE COUNT 7 a 6 c 5 g 4 t
 ORIGIN

Query Match 44.7%; Score 13.4; DB 6; Length 25;
 Best Local Similarity 79.0%; Pred. No. 1 20000;
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Dels 0

QY 2 TATTCGAGAGAGATGTT 24
 |||||
 DP 23 TATTCGAGAGAGATGTT 24

RESULT 32
 AR198271
 LOCUS AR198271 28 bp. DNA
 DEFINITION AR198271
 ACCESSION AR198271
 VERSION AR198271.1 GI:22245120
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 28)
 AUTHORS Chenchik, A., Jekhadze, G. and Bihlachevillir, R.
 TITLE Methods of assaying differential expression
 JOURNAL Patent: US 590476-A 1999 30-NOV-1999;
 FEATURES
 SOURCE Location/Qualifiers
 1..28

BASE COUNT 7 a 8 c 5 g 9 t
 ORIGIN

Query Match 44.7%; Score 13.4; DB 6; Length 25;
 Best Local Similarity 79.0%; Pred. No. 1 20000;
 Matches 17, Conservative 0, Mismatches 0, Indels 0, Dels 0

QY 2 TATTCGAGAGAGATGTT 24
 |||||
 DP 23 TATTCGAGAGAGATGTT 24

DP 23 TATTCGAGAGAGATGTT 24

RESULT 32
 AR047999
 LOCUS AR047999 21 bp. DNA
 DEFINITION AR047999
 ACCESSION AR047999
 VERSION AR047999.1 GI:10000000
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Palase, P. and Garcia-Sastre, A.
 TITLE Influenza virus RNA virus expression systems and vaccines
 JOURNAL Patent: US 5820871-A 1 13-OCT-1998;
 FEATURES
 SOURCE Location/Qualifiers
 1..21

BASE COUNT 6 a 3 c 5 g 7 t
 ORIGIN

Query Match 44.0%; Score 13.2; DB 6; Length 25;
 Best Local Similarity 81.3%; Pred. No. 2 20005;
 Matches 15, Conservative 0, Mismatches 1, Indels 0, Dels 0

QY 12 AGAGAGATGTTCTGTT 29
 |||||
 DP 2 AGAGAGATGTTCTGTT 19

RESULT 34
 AR068627
 LOCUS AR068627 25 bp. DNA
 DEFINITION AR068627
 ACCESSION AR068627
 VERSION AR068627.1 GI:10000000
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Palase, P. and Garcia-Sastre, A.
 TITLE Influenza virus RNA virus expression systems and vaccines
 JOURNAL Patent: US 5820871-A 1 13-OCT-1998;
 FEATURES
 SOURCE Location/Qualifiers
 1..21

BASE COUNT 6 a 3 c 5 g 7 t
 ORIGIN

Query Match 44.0%; Score 13.2; DB 6; Length 25;
 Best Local Similarity 81.3%; Pred. No. 2 20005;
 Matches 15, Conservative 0, Mismatches 1, Indels 0, Dels 0

QY 12 AGAGAGATGTTCTGTT 29
 |||||
 DP 2 AGAGAGATGTTCTGTT 19

RESULT 35
 AR094235
 LOCUS AR094235 21 bp. DNA
 DEFINITION AR094235
 ACCESSION AR094235
 VERSION AR094235.1 GI:10000000
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 21)
 AUTHORS Palase, P. and Garcia-Sastre, A.
 TITLE Influenza virus RNA virus expression systems and vaccines
 JOURNAL Patent: US 5820871-A 1 13-OCT-1998;
 FEATURES
 SOURCE Location/Qualifiers
 1..21

BASE COUNT 6 a 3 c 5 g 7 t
 ORIGIN

Query Match 44.0%; Score 13.2; DB 6; Length 25;
 Best Local Similarity 81.3%; Pred. No. 2 20005;
 Matches 15, Conservative 0, Mismatches 1, Indels 0, Dels 0

QY 12 AGAGAGATGTTCTGTT 29
 |||||
 DP 2 AGAGAGATGTTCTGTT 19

Source

1..28

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BASE COUNT 9 a 4 c 11 g 4 t

ORIGIN

Query Match 46.0% Score 13.9; DB 6; Length 29;
 Best Local Similarity 88.2% Pred. No. 1,26+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 TGGCGACGAGCAATG 22
 ||||| ||||| |||||
 5 TGGCGACGAGCAATG 21

RESULT 26

LOCUS AR122854 29 bp DNA linear PAT 16 MAY 2001
 DEFINITION Sequence 74 from patent US 6168778.
 ACCESSION AR122854
 VERSION AR122854.1 GI:14107816
 KEYWORDS

SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 29)
 Jancic,N., Gold,L., Schmidt,P. and Vargese,G.
 Vascular endothelial growth factor (VEGF) Nucleic Acid Induced
 Complexes
 Patent: US 6168778 A 74 02 JAN 2001;
 Location/Qualifiers
 1..29
 /organism="unknown"

BASE COUNT 9 a 4 c 12 g 4 t

ORIGIN

Query Match 46.0% Score 13.9; DB 6; Length 29;
 Best Local Similarity 88.2% Pred. No. 1,26+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 TGGCGACGAGCAATG 22
 ||||| ||||| |||||
 6 TGGCGACGAGCAATG 22

RESULT 27

LOCUS AR122853 29 bp DNA linear PAT 16 MAY 2001
 DEFINITION Sequence 75 from patent US 6168778.
 ACCESSION AR122853
 VERSION AR122853.1 GI:14107817
 KEYWORDS

SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 29)
 Jancic,N., Gold,L., Schmidt,P. and Vargese,G.
 Vascular endothelial growth factor (VEGF) Nucleic Acid Induced
 Complexes
 Patent: US 6168778 A 75 02 JAN 2001;
 Location/Qualifiers
 1..29
 /organism="unknown"

BASE COUNT 9 a 4 c 12 g 4 t

ORIGIN

Query Match 46.0% Score 13.9; DB 6; Length 29;
 Best Local Similarity 88.2% Pred. No. 1,26+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 TGGCGACGAGCAATG 22
 ||||| ||||| |||||
 6 TGGCGACGAGCAATG 22

RESULT 28

LOCUS AR122854 29 bp DNA linear PAT 16 MAY 2001
 DEFINITION Sequence 76 from patent US 6168778.
 ACCESSION AR122854
 VERSION AR122854.1 GI:14107820
 KEYWORDS

SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 29)
 Jancic,N., Gold,L., Schmidt,P. and Vargese,G.
 Vascular endothelial growth factor (VEGF) Nucleic Acid Induced
 Complexes
 Patent: US 6168778 A 76 02 JAN 2001;
 Location/Qualifiers
 1..29
 /organism="unknown"

BASE COUNT 9 a 4 c 12 g 4 t

ORIGIN

Query Match 46.0% Score 13.9; DB 6; Length 29;
 Best Local Similarity 88.2% Pred. No. 1,26+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 TGGCGACGAGCAATG 22
 ||||| ||||| |||||
 6 TGGCGACGAGCAATG 22

RESULT 29

LOCUS AR122855 29 bp DNA linear PAT 16 MAY 2001
 DEFINITION Sequence 77 from patent US 6168778.
 ACCESSION AR122855
 VERSION AR122855.1 GI:14107821
 KEYWORDS

SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 29)
 Jancic,N., Gold,L., Schmidt,P. and Vargese,G.
 Vascular endothelial growth factor (VEGF) Nucleic Acid Induced
 Complexes
 Patent: US 6168778 A 77 02 JAN 2001;
 Location/Qualifiers
 1..29
 /organism="unknown"

BASE COUNT 9 a 4 c 12 g 4 t

ORIGIN

Query Match 46.0% Score 13.9; DB 6; Length 29;
 Best Local Similarity 88.2% Pred. No. 1,26+05;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

6 TGGCGACGAGCAATG 22
 ||||| ||||| |||||
 6 TGGCGACGAGCAATG 22

RESULT 30

LOCUS AR122853 29 bp DNA linear PAT 16 MAY 2001
 DEFINITION Sequence 55 from patent US 6168778.
 ACCESSION AR122853
 VERSION AR122853.1 GI:14107799
 KEYWORDS

SOURCE
 ORGANISM
 Unclassified.
 1 (bases 1 to 30)
 Jancic,N., Gold,L., Schmidt,P. and Vargese,G.

BASE COUNT 9 a 4 c 12 g 4 t

Best Loc 17: 46.0% Score 13.8; DB 6; Length 28;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0.

CY 7 GCGGACGAGGAGATGCTTTC 28
|||||
DB 22 GCTGACGAGGAGATGCTTTC 1

RESULT 21
LOCUS 186340/c 21 bp DNA linear EXT 10 MAY 1998
DEFINITION Sequence 75 from patent US 5700997.
ACCESSION 186340
VERSION 186340.1 GI:1426088
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 24)
Hersend, T., Tishbel, F., Pagan, P., and Patisson, J.
Nucleotide sequences coding for variable regions of human chaperone of human T lymphocyte receptors, differentially peptide segments and the diagnostic and therapeutic uses
Patent: US 5700997-A (5/23/98-1997)
Location/Qualifiers
1..24
/organism="Unknown"

BASE COUNT 6 a 9 c 3 g 6 t

ORIGIN
Query Match 46.0% Score 13.8; DB 6; Length 28;
Best Local Similarity 98.2% Ext: No. 126405;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0.

CY 7 GCGGACGAGGAGATGCTTTC 28
|||||
DB 22 GCTGACGAGGAGATGCTTTC 1

RESULT 22
LOCUS AR11122/c 25 bp DNA linear EXT 10 MAY 2001
DEFINITION Sequence 17 from patent US 5700997.
ACCESSION AR11122
VERSION AR11122.1 GI:14119447
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 25)
Kong, H., Higgins, J., Dalton, M., Murrell, P. and Smith, P.
Cloning and producing the N-BENED1 nucleic acid sequence
Journal Patent: US 5700997-A (5/23/98-1997)
Location/Qualifiers
1..25
/organism="Unknown"

BASE COUNT 7 a 8 c 4 g 6 t

ORIGIN
Query Match 46.0% Score 13.8; DB 6; Length 28;
Best Local Similarity 98.2% Ext: No. 126405;
Matches 17; Conservative 0; Mismatches 5; Indels 0; Gaps 0.

CY 6 TGGGACGAGGAGATGCTTTC 27
|||||
DB 24 TGGGACGAGGAGATGCTTTC 3

RESULT 23
LOCUS AM22293 23 bp DNA linear EXT 02 NOV 2001
DEFINITION Sequence 13 from patent WO/99/01443A.
ACCESSION AM22293
VERSION AM22293.1 GI:1426088
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 23)
Kong, H., Higgins, J., Dalton, M., Murrell, P. and Smith, P.
Cloning and producing the N-BENED1 nucleic acid sequence
Journal Patent: US 5700997-A (5/23/98-1997)
Location/Qualifiers
1..23
/organism="Unknown"

VERSION AM22293.1 GI:1426088
KEYWORDS
SOURCE
ORGANISM
REFERENCE
1 (bases 1 to 23)
Zehender, B., Lasser-Pell, U. and Fritschner, H.
Methods and compositions for regulating adipocytes
Patent: WO 99/01443A (3/07-SEP-2001)
Location/Qualifiers
1..23
/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer"

BASE COUNT 5 a 2 c 10 g 6 t

ORIGIN
Query Match 46.0% Score 13.8; DB 6; Length 28;
Best Local Similarity 98.2% Ext: No. 126405;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

CY 9 GCGGACGAGGAGATGCTTTC 25
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DB 6 GCGGACGAGGAGATGCTTTC 22

RESULT 24
LOCUS AR122834 28 bp DNA linear EXT 10 MAY 2001
DEFINITION Sequence 56 from patent US 5700997.
ACCESSION AR122834
VERSION AR122834.1 GI:14107800
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 28)
Janjic, N., Gold, L., Schmidt, P. and Vargese, J.
Vascular endothelial growth factor (VEGF) Nucleic Acid and
Complexes
Patent: US 5700997-A (5/23/98-1997)
Location/Qualifiers
1..28
/organism="Unknown"

BASE COUNT 9 a 3 c 12 g 4 t

ORIGIN
Query Match 46.0% Score 13.8; DB 6; Length 28;
Best Local Similarity 98.2% Ext: No. 126405;
Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0.

CY 6 TGGGACGAGGAGATGCTTTC 22
|||||
DB 6 TGGGACGAGGAGATGCTTTC 22

RESULT 25
LOCUS AR122835 28 bp DNA linear EXT 10 MAY 2001
DEFINITION Sequence 56 from patent US 5700997.
ACCESSION AR122835
VERSION AR122835.1 GI:14107801
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 28)
Janjic, N., Gold, L., Schmidt, P. and Vargese, J.
Vascular endothelial growth factor (VEGF) Nucleic Acid and
Complexes
Patent: US 5700997-A (5/23/98-1997)
Location/Qualifiers
1..28
/organism="Unknown"

FEATURES
Source
Location/Qualifiers
1..30
/organism="Synthetic Construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT
10 a 10 c 4 g 6 t

Query Match
Best Local Similarity 100.0% Score 30; DB 6; Length 30;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 4
AX032830
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AX032830
Sequence 1 from Patent WO004446
AX032830.1 GI:10279897
Synthetic construct.
Synthetic construct.
artificial sequences.
1 (bases 1 to 30)
Baker, D.L. and Green, C.B.
Formulations comprising antisense nucleotides to connexins
Patent: WO 004446 A1 (1999-09-09)
Baker, David Lawrence (DB) ; Green, Colin Richard (NZ)

FEATURES
Source
Location/Qualifiers
1..30
/organism="Synthetic Construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT
8 a 4 c 9 g 10 t

Query Match
Best Local Similarity 93.3% Score 28; DB 6; Length 30;
Matches 28; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 5
AX032830
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AX032830
Sequence 8 from Patent WO004446
AX032830.1 GI:10279894
Synthetic construct.
Synthetic construct.
artificial sequences.
1 (bases 1 to 30)
Baker, D.L. and Green, C.B.
Formulations comprising antisense nucleotides to connexins
Patent: WO 004446 A1 (1999-09-09)
Baker, David Lawrence (DB) ; Green, Colin Richard (NZ)

FEATURES
Source
Location/Qualifiers
1..30
/organism="Synthetic Construct"
/db_xref="taxon:32630"
/note="Oligonucleotide"

BASE COUNT
7 a 5 c 12 g 4 t

FEATURES
Source
Location/Qualifiers
1..28
/organism="Synthetic Construct"
/db_xref="taxon:32630"

BASE COUNT
7 a 5 c 12 g 4 t

Query Match
Best Local Similarity 91.8% Score 12; DB 6; Length 28;
Matches 18; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 7
AX447308
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AX447308
Sequence 3763 from Patent WO0216649.
AX447308.1 GI:10692197
Synthetic construct.
Synthetic construct.
artificial sequences.
1
Gundersen, K.
Patent: WO 0216649 A1 (2002-02-28)
Alumina, Inc. (US)

FEATURES
Source
Location/Qualifiers
1..24

RESULT 6
E38328
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

E38328
Process for producing L-methionine by fermentation.
E38328
E38328.1 GI:18624940
JP 2000139471-A/1.
Synthetic construct.
Synthetic construct.
artificial sequences.
1 (bases 1 to 48)
Gutari, Y. and Kurahashi, O.
Process for producing L-methionine by fermentation
Patent: JP 2000139471 A 1 23 MAY 2000;
Ajinomoto Co Inc
CN Official S-Sequence
EN JP 2000139471-A/1
FD 23 MAY 2000
HP 17 NOV 1999 JP 1999226717
FR

ROSHIKO USUI/AOSAMU KURAHASHI
J. CHEM. SOC., CHEM. COMMUN., 1999, 1209-1210
DOI: 10.1039/A800013G

FEATURES
Source
Location/Qualifiers
1..28
/organism="Artificial Sequence"

BASE COUNT
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C 944	10.6	35.3	20	6	AX018901	AX018901 Sequence
C 945	10.6	35.3	20	6	AX018916	AX018916 Sequence
C 946	10.6	35.3	20	6	AX019030	AX019030 Sequence
C 947	10.6	35.3	20	6	AX021180	AX021180 Sequence
C 948	10.6	35.3	20	6	AX031457	AX031457 Sequence
C 949	10.6	35.3	20	6	AX149017	AX149017 Sequence
C 950	10.6	35.3	20	6	AX149042	AX149042 Sequence
C 951	10.6	35.3	20	6	AX149131	AX149131 Sequence
C 952	10.6	35.3	20	6	AX293367	AX293367 Sequence
C 953	10.6	35.3	20	6	AX320843	AX320843 Sequence
C 954	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 955	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 956	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 957	10.6	35.3	20	6	AX447634	AX447634 Sequence
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C 959	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 960	10.6	35.3	20	6	AX447634	AX447634 Sequence
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C 963	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 964	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 965	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 966	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 967	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 968	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 969	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 970	10.6	35.3	20	6	AX447634	AX447634 Sequence
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C 972	10.6	35.3	20	6	AX447634	AX447634 Sequence
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C 976	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 977	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 978	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 979	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 980	10.6	35.3	20	6	AX447634	AX447634 Sequence
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C 994	10.6	35.3	20	6	AX447634	AX447634 Sequence
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C 996	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 997	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 998	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 999	10.6	35.3	20	6	AX447634	AX447634 Sequence
C 1000	10.6	35.3	20	6	AX447634	AX447634 Sequence

ALIGNMENTS

RESULT 1
LOCUS AX018859 30 bp DNA linear PAT 21 SEP 2000
DEFINITION Sequence 1 from Patent WO0044409.
ACCESSION AX018859
VERSION AX018859.1 GI:102798
KEYWORDS
SOURCE Synthetic construct.
ORGANISM *Escherichia coli*

REFERENCE
1 (bases 1 to 30)
Becker, D.L. and Green, C.R.
Formulations comprising antisense nucleotides to hepatitis B virus
Patent: WO 0044409-A 2 (31-Aug-2000)
BECKER, DAVID LAWRENCE (GB); GREEN, CLIVE RICHARD (GB)
(NZ)

FEATURES
Source
1 to 30
Location/Qualifiers
/db:taxid="taxon:32830"
/db:taxid="taxon:32830"

BASE COUNT
6 a 4 c 10 g 10 t

Query Match 100.0% Score 30.0 DB 6 Length 30
Post-local similarity: 100.0% (E=0.000)
Matches: 30 Conserved: 30 of 30 Mismatches: 0 of 0 Gaps: 0 of 0

CY
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|||||
1 GATATGCGGAGAGAAATGTTCTGTC 30

RESULT 2
LOCUS AX018859 30 bp DNA linear PAT 21 SEP 2000
DEFINITION Sequence 1 from Patent WO0044409.
ACCESSION AX018859
VERSION AX018859.1 GI:102798
KEYWORDS
SOURCE Synthetic construct.
ORGANISM *Escherichia coli*

REFERENCE
1 (bases 1 to 30)
Becker, D.L. and Green, C.R.
Formulations comprising antisense nucleotides to hepatitis B virus
Patent: WO 0044409-A 2 (31-Aug-2000)
BECKER, DAVID LAWRENCE (GB); GREEN, CLIVE RICHARD (GB)
(NZ)

FEATURES
Source
1 to 30
Location/Qualifiers
/db:taxid="taxon:32830"
/db:taxid="taxon:32830"

BASE COUNT
10 a 10 c 4 g 6 t

CY
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|||||
1 GATATGCGGAGAGAAATGTTCTGTC 30

RESULT 3
LOCUS AX018859 30 bp DNA linear PAT 21 SEP 2000
DEFINITION Sequence 1 from Patent WO0044409.
ACCESSION AX018859
VERSION AX018859.1 GI:102798
KEYWORDS
SOURCE Synthetic construct.
ORGANISM *Escherichia coli*

REFERENCE
1 (bases 1 to 30)
Becker, D.L. and Green, C.R.
Formulations comprising antisense nucleotides to hepatitis B virus
Patent: WO 0044409-A 2 (31-Aug-2000)
BECKER, DAVID LAWRENCE (GB); GREEN, CLIVE RICHARD (GB)
(NZ)

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359	11.4	38.0	30.6	AX389845	Sequence	432	11.2	37.3	25.6	E19912	Sequence
360	11.4	38.0	30.6	AX389845	Sequence	433	11.2	37.3	25.6	E19912	Sequence
361	11.4	38.0	30.6	AX389845	Sequence	434	11.2	37.3	25.6	E19912	Sequence
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363	11.4	38.0	30.6	AX389845	Sequence	436	11.2	37.3	25.6	E19912	Sequence
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366	11.4	38.0	30.6	AX389845	Sequence	439	11.2	37.3	25.6	E19912	Sequence
367	11.4	38.0	30.6	AX389845	Sequence	440	11.2	37.3	25.6	E19912	Sequence
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373	11.4	38.0	30.6	AX389845	Sequence	446	11.2	37.3	25.6	E19912	Sequence
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379	11.4	38.0	30.6	AX389845	Sequence	452	11.2	37.3	25.6	E19912	Sequence
380	11.4	38.0	30.6	AX389845	Sequence	453	11.2	37.3	25.6	E19912	Sequence
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383	11.4	38.0	30.6	AX389845	Sequence	456	11.2	37.3	25.6	E19912	Sequence
384	11.4	38.0	30.6	AX389845	Sequence	457	11.2	37.3	25.6	E19912	Sequence
385	11.4	38.0	30.6	AX389845	Sequence	458	11.2	37.3	25.6	E19912	Sequence
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389	11.4	38.0	30.6	AX389845	Sequence	462	11.2	37.3	25.6	E19912	Sequence
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391	11.4	38.0	30.6	AX389845	Sequence	464	11.2	37.3	25.6	E19912	Sequence
392	11.4	38.0	30.6	AX389845	Sequence	465	11.2	37.3	25.6	E19912	Sequence
393	11.4	38.0	30.6	AX389845	Sequence	466	11.2	37.3	25.6	E19912	Sequence
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395	11.4	38.0	30.6	AX389845	Sequence						

SUMMARY

Prod. No. is the number of results predicted by chance to have a

Result No.	Score	Query Match	Length	DB	ID	Description
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2	48	100%	20	6	AX12624	AX12624 Sequence
3	30	100%	30	6	AX03883	AX03883 Sequence
4	26	98%	30	6	AX03883	AX03883 Sequence
5	20	98%	30	6	AX03883	AX03883 Sequence
6	15	98%	24	6	AX447108	AX447108 Sequence
7	15	98%	24	6	AX447108	AX447108 Sequence
8	15	98%	24	6	AX447108	AX447108 Sequence
9	15	98%	24	6	AX447108	AX447108 Sequence
10	14	98%	30	6	AX107179	AX107179 Sequence
11	14	98%	30	6	AX107179	AX107179 Sequence
12	14	98%	30	6	AX107179	AX107179 Sequence
13	14	98%	30	6	AX107179	AX107179 Sequence
14	14	98%	30	6	AX107179	AX107179 Sequence
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64	14	98%	30	6	AX107179	AX107179 Sequence
65	14	98%	30	6	AX107179	AX107179 Sequence

TITLE

Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL

Plasmid inserts

Unpublished (2000)

Contact: Robert B. Weiss

University of Utah Genome Center

Bldg. 308, Rm. 308, 1100 E. 1000 S., Salt Lake City, UT 84112, USA

Tel: 801 585 5606

Fax: 801 585 7177

Email: dunn@genetics.utah.edu

Insert length: 10000 Std Error: 0.00

Plate: 0406 Row: K Column: 12

Seq primer: GATACAG-3AACAAGTATGAC

Class: plasmid ends

FEATURES

High quality sequence stop: 34.

Location/Qualifiers

1..34

/organism="Mus musculus"

/strain="C57BL/6J"

/db_xref="taxon:10090"

/clone="MIM0306K12"

/clone_id="Mouse 10kb plasmid MIM0306K12"

/sex="Male"

/lab_host="E. coli strain X10-Gold, Ti-resistant, F-"

/note="Vector: pMD201; Full-length genomic DNA from M. musculus (MIM0306K12) was obtained from the Jackson Laboratory mouse DNA resource

(http://www.jax.org/resources/documents/notes/). The DNA

was hydrolytically sheared by repeated passage through a

0.005 inch orifice at constant velocity. The sheared DNA

was blunt end-repaired with T4 DNA polymerase and T4

polynucleotide kinase. Adaptor oligonucleotides were

ligated to the blunt ends in high molar excess. The

adaptor RNA was purified and size-selected for a 9.5 to

10.5 kb range using preparative agarose gel

electrophoresis. Vector RNA was prepared from a derivative

of pMD201 (41472114/2b/AP12922.1), a copy-number

inducible derivative of plasmid p1. The vector was ligated

with adaptors complementary to the insert adaptors and

purified. The sheared, adaptor mouse DNA was annealed to

adaptor vector DNA, and transformed into

chemically-competent E. coli X10-Gold (Stratagene) cells

and selected for ampicillin resistance."

BASE COUNT

11 a 7 c 5 g 11 t

ORIGIN

Query Match 39 74 Score 11.67 PP 17 Length 34

Best Local Similarity 77.8% Freq. No. 1.2e-06

Matches 14; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 12 AAGAGAAATGTTCTCT 29

DB 29 AAGAGAAATGTTCTCT 12

Search completed: July 21, 2003, 15:46:38
Job time: 402.76 secs

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DEFINITION   AAT95869.1 nt: cDNA unpublished DNA library from intestinalis
ACCESSION   A075869
VERSION     A075869.1
KEYWORDS    EST
ORGANISM    Clona intestinalis
REFERENCE   1. Sakai, N., Satoh, Y., Kohara, Y., and Shin-i, T.
            Expressed genes in Clona intestinalis
            Unpublished (2000)
AUTHORS     Sach,N., Satoh,Y., Kohara,Y. and Shin-i,T.
TITLE       Expressed genes in Clona intestinalis
JOURNAL     Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto 606-8501, Japan
            Tel: 81-75-753-4061
            Fax: 81-75-705-1119
            Email: satoh@zoology.kyoto-u.ac.jp
FEATURES             Source
                     1..34
                     /organism="Clona intestinalis"
                     /db_xref="taxid:5793"
                     /clone="cld13022"
                     /tissue_type="whole animal"
                     /dev_stage="adult"
                     /note="uncloned; prepared by SK"
BASE COUNT      4 A          3 C          3 G          10 T
ORIGIN
Query Map...           3673; Score 11.67; E=1e-34; Length 34;
Best local similarity 60.0%, full mismatched 0%
Matches: 17; Conserving: 0; Mismatched: 0; Indels: 0; Gaps: 0
QY
1 ATGTTTAAATAAATTCTGTCTG 20
+|||||||+|||||||+
2 AATGGGCAAGAGCGCTTTTTTT 27
+|||||||+|||||||+
DEFINITION   AAT95354.1 nt: cDNA unpublished DNA library from intestinalis
ACCESSION   A075869
VERSION     A075869.1
KEYWORDS    EST
ORGANISM    Clona intestinalis
REFERENCE   1. Sakai, N., Satoh, Y., Kohara, Y., and Shin-i, T.
            Expressed genes in Clona intestinalis
            Unpublished (2000)
AUTHORS     Sach,N., Satoh,Y., Kohara,Y. and Shin-i,T.
TITLE       Expressed genes in Clona intestinalis
JOURNAL     Unpublished (2000)
COMMENT     Contact: Nori Satoh
            Department of Zoology
            Kyoto University
            Sakyo-ku, Kyoto 606-8501, Japan
            Tel: 81-75-753-4061
            Fax: 81-75-705-1119
            Email: satoh@zoology.kyoto-u.ac.jp
FEATURES             Source
                     1..34
                     /organism="Clona intestinalis"
                     /db_xref="taxid:5793"
                     /clone="cld13022"
                     /tissue_type="whole animal"
                     /dev_stage="adult"
                     /note="uncloned; prepared by SK"

```

[illegible]

University of Utah Genome Center
 University of Utah
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 1400 E., Salt Lake City, UT 84143, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu

Insert Length: 10000 Std Error: 0.00
 Plate: 0428 row: M column: 22
 Seq Primer: CACACAGCAGAACAGCATATGACG
 Class: plasmid ends
 High quality sequence steps: 29.

FEATURES

Source

1..29

Location/Qualifiers

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U05C1M0528M22"
 /clone_lib="mouse jvark plasmid library"
 /sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMW429v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/downloads/dnares/>) The DNA was hydrolytically sheared by repeated passage through a 20-gauge needle and ligated with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter DNA was purified and size-selected for a 3.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD19-LT (Life Technologies), a 3.7-kb-number-11 derivative of plasmid p1. The vector was ligated with adapters complementary to the insert adapters and purified. The sheared, adapter mouse DNA was annealed to adapter vector DNA and transformed into chemically competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

BASE COUNT

4 A 12 C 3 G 10 T

ORIGIN

Query March 19 38; Score 11.8; DB 9; Length 67
 Best Local Similarity 86.78; Pval No. 1.3e-05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 7 GACGACAGACAAATT 21
 1 ||||| |||||

Db 26 GACGACAGACAAATT 12

RESULT 25
 A0244502.6
 LOCUS A0244502.6 10 bp mRNA EST 25-APR-2002
 DEFINITION A0244502.6 10 bp mRNA library Mus musculus cDNA clone
 HED0002277.1, mRNA sequence.

ACCESSION A0244502
 A0244502.1 GI:20316343

KEYWORDS EST

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

COMMENT

Generation of expressed sequence tags from mouse brain
 Kato, F. and M. H. F.
 Genomics 2002, 49:1-10
 GenBank accession: A0244502.6
 Nara Institute of Biomedical Sciences
 8916-5 Takayama, Ikoma, Nara 630-0101, Japan
 Tel: 81-743-72 5581

Fax: 81 743 72 5589
 Email: kato@nibs.nara.ac.jp,
 m.h.f@nibs.nara.ac.jp
 Location/Qualifiers

FEATURES

Source

1..30

Location/Qualifiers

/organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="U05C1M02277"
 /clone_lib="3'-directed mouse cDNA library"
 /tissue_type="brain"
 /note="Vector: pGEM-T-easy"

BASE COUNT

10 A 7 C 5 G 8 T

ORIGIN

Query March 19 38; Score 11.8; DB 9; Length 67
 Best Local Similarity 86.78; Pval No. 1.3e-05;
 Matches 13; Conservative 0; Mismatches 2; Indels 0; Gaps 0

QY 5 TTGCGACAGACAAATTGTTT 27
 1 ||||| ||||| |||||

Db 30 TTGCGACAGACAAATTGTTT 8

RESULT 26
 A0244505
 LOCUS A0244505 10 bp mRNA EST 25-APR-2002
 DEFINITION A0244505 10 bp mRNA library Mus musculus cDNA clone
 HED0002277.1, mRNA sequence.

ACCESSION A0244505
 A0244505.1 GI:10546418

KEYWORDS

SOURCE

ORGANISM

Mus musculus

REFERENCE

AUTHORS

TITLE

COMMENT

Mouse whole genome scaffolding with paired end reads from 10K
 plasmid inserts
 Published (2000)
 Contact: Robert P. Weiss
 University of Utah Genome Center
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 1400 E., Salt Lake City, UT 84143, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: ddunn@genetics.utah.edu
 Insert Length: 10000 Std Error: 0.00
 Plate: 0201 row: 0 column: 04
 Seq Primer: GATTGTAAAGAACGAGCAT
 Class: plasmid ends
 High quality sequence steps: 30.
 Location/Qualifiers

1..30

/organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /clone="U05C1M0201004"
 /clone_lib="3'-directed mouse cDNA library"
 /sex="Male"

/lab_host="E. coli strain XL10-Gold, T1-resistant, F-"
 /note="Vector: PMW429v; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/downloads/dnares/>) The DNA was hydrolytically sheared by repeated passage through a 20-gauge needle and ligated with T4 DNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were

University of Utah Genome Center
 University of Utah
 RM 308, E. North Campus Research Bldg., 20 S. 1400 E., Ste. 300
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 1000 bp
 Plate: 0274 row: 6 column: 01
 Seq primer: CGTTGTAACAGCAAGCGACAGT
 Class: plasmid ends
 High quality sequence step: 25
 Location: Qualifiers
 1. 35
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /cdate="200206270000"
 /cversion="1.0.0"
 /sex="Female"

BASE COUNT
 ORIGIN
 10 a 12 c 2 g 11 t
 Query Match 46 38 Score 100 Length 25
 Best local similarity 64.8% (E=0.000000)
 Mismatches 10, Indels 0, Matches 15, 16 bp
 2 TAATGCGGACAGAGATGCTTCT 29
 34 TACATGAGGAGAAAGAAATTTTCT 7

RESULT 23
 AZ473354/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCES
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

University of Utah Genome Center
 University of Utah
 RM 308, E. North Campus Research Bldg., 20 S. 1400 E., Ste. 300
 84112, USA
 Tel: 801 585 5606
 Fax: 801 585 7177
 Email: dunn@genetics.utah.edu
 Insert Length: 1000 bp
 Plate: 0274 row: 6 column: 08
 Seq primer: CGTTGTAACAGCAAGCGACAGT
 Class: plasmid ends
 High quality sequence step: 26
 Location: Qualifiers
 1. 26
 /organism="Mus musculus"
 /strain="C57BL/6J"
 /db_xref="taxon:10090"
 /cdate="200206270000"
 /cversion="1.0.0"
 /sex="Male"

BASE COUNT
 ORIGIN
 10 a 6 c 3 g 7 t
 Query Match 53.6% Score 100 Length 26
 Best local similarity 69.6% (E=0.000000)
 Mismatches 10, Indels 0, Matches 17, 18 bp
 3 AATGCGGACAGAGATGCTTCT 25
 24 AATGCGGACAGAGATGCTTCT 2

RESULT 24
 AZ654659/c
 LOCUS
 DEFINITION
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCES
 AUTHORS
 TITLE
 JOURNAL
 COMMENT

SOURCE
ORGANISM
Mus musculus
house mouse

REFERENCE
AUTHORS
Dumortier, C., Wenzel, A., Chertova, G., Vozokhina, E., Polozhentsev,
Mamajima, T., Fothergill, J., Podewils, L., Schürmann, M., Müller,
I. (bases 1 to 33)
Dumortier, C., Wenzel, A., Balthasar, M., Schürmann, T., Duvall, R., Hamill, C.,
Jensen, H., Longaker, S., Mahmood, M., Meentemeyer, E., Podewils, T., Bell,
M., Rosen, M., Rosen, P., Stokes, F., Tinjuy, A., van Nieuwenhuizen, A.
and Wright, D., Weiss, F.

TITLE
Mouse whole genome scaffolding with paired end reads from 10Xb
Plasmid inserts

JOURNAL
Unpublished (2008)

COMMENT
Contact: Robert B. Weiss
University of Utah Cancer Center
University of Utah
Rm. 302, Field Medical Sciences Research Bldg., 20 E. 2000 E., Salt Lake City,
84112, USA
Tel.: 801 585 5606
Fax: 801 595 7173
Email: dham@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0069 ROW: F Column: 10
Seq-Project: TCACAG336AAATGACTA3AC
Class: Plasmid ends
High quality sequence stops: 33.
Location/Qualifiers
1..33
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10088"
/contig="mmcgwmoacrfp0"
/feature="init" "m use init plasmid vector library"
/name="Mouse"
/lab_host="E. coli strain XL10 gold, pT resistant, F+ "
/date="Vector PCR-ready, Purified plasmid DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (<http://www.jax.org/resources/documents/dnares/>). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-ligated with Ta RNA polymerase and T4 polynucleotide kinase. Adapter oligonucleotides were ligated to the blunt ends in high molar excess. The adapter cDNA was purified and size selected for a 2.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector cDNA was prepared from a derivative of pmw42 (gi|4732143gb|AF12972.1), a copy-number inducible derivative of plasmid p1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared adaptor mouse cDNA was annealed to adapted vector cDNA, and transformed into chemically competent E. coli XL10 Gold (Stratagene) cells and selected for ampicillin resistance."

PHASE COUNT
ORIGIN
10 a 1 g 11 f 11 t

Query Match 41 3% Score 12.4 DB 17 Length 33:
Best Local Similarity 72 7% Read No. 566001
Matches 14 Coverage 72 % Mismatch 0 Indels 0 Gaps 0

CY 1 GTATTGTGGCCAGAAGTAATG 22
||||||| ||| |
1 GTATTGTGCCTGATAAATG 22

DB 1

RESULT 10
LOCUS C00576/c
DEFINITION Human chromosome 17 chr17: 11,000,000-11,000,000 bp
ACCESSION NC_00576
VERSION 2
KEYWORDS EST

SOURCE human.
 ORGANISM Homo sapiens.
 Eukaryotic. Mammalia. Primates. Catarrhini. Hominoidea. Hominidae.
 REFERENCE 1 (bases 1 to 27)
 AUTHORS Okiubo, K.
 TITLE Poly(A) human gene expression database
 JOURNAL Unpublished (1995)
 COMMENT Contact: Okubo, K.
 Institute for Molecular and Cellular Biol
 Osaka University
 1-1, Yamadaoka, Suita, Osaka Pref. 565, Japan
 Tel: 06-877-5111(ex.315)
 Email: yamadaoka@f.mri.ac.jp
 Human Gene Signature, 3'-directed cDNA sequence. We are now
 submitting the above cDNA sequence redundantly to EMBL, GenBank,
 For the abundance information of clones with this sequence in this
 library and as well as in other 3'-directed libraries, see
 http://www.imb.hokkaido.ac.jp/hgdb/. The sequences of the clones
 represented by this cDNA sequences is also found there.
 location/Qualifiers
 1..27
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cve_full="human adult (K Okiubo)"
 /dev_stage="adult"
 /note="Organic blood. Vectors: lenti-11. Site: 1. EMBL
 Monocytes were prepared from blood by Ficoll gradient,
 Percoll and T cell selecting purification steps finally
 a T cell RNA was isolated from activated monocytes from a
 patient with rheumatoid arthritis. mRNA was reverse
 transcribed with poly(A) using first-strand cDNA was
 cloned into lenti-11 vector arms. The cDNA library was
 screened by differential hybridization using radiolabeled cDNA
 methylase cDNA from activated and non activated
 monocytes.
 " 3 g 9 t
 BASE COUNT 13 a 3 g 9 t
 ORIGIN
 Query March 48 78 Score 12.3 DB 14 Length 27
 Pos: 13.31 identity 92.4% Pos: 13.31 72.0%
 Matches 14 Conservative 0 Mismatches 3 Indels 0 gaps 0
 27 13 AAGAGATCTCTCTCT 29
 ++++++
 71 AAGAGATTTCTTT 5
 RESULT 11
 B0419809 33 bp mRNA lncRNA EST 14 MAR 2000
 REFERENCE 1 NIH-MGC 11 Human sapiens cDNA clone (AAB044019) v.
 cDNA sequence.
 B0419809
 ACCESSION B0419809.1 GI:13326315
 VERSION EST.
 KEYWORDS human.
 SOURCE human.
 ORGANISM Homo sapiens.
 Eukaryotic. Mammalia. Primates. Catarrhini. Hominoidea. Hominidae.
 REFERENCE 1 (bases 1 to 33)
 AUTHORS NIH-MGC HALLP:/mgs.nhl.nih.gov/.
 TITLE NIH-MGC HALLP:/mgs.nhl.nih.gov/.
 JOURNAL National Institutes of Health, Human Gene Collection (MTC)
 Unpublished (1999)
 COMMENT Contact: Robert Stransberg, Ph.D.
 Email: cga@gsf.rem.nhl.nih.gov
 Tissue Procurement: DCTD/DRP
 cDNA library prepared using High-capacity library
 cDNA library Arrayed by The IMAGE Consortium (IMAGE)
 cDNA Sequenced by InCyte Genomics, Inc.
 clone identifier: MGC clone distribution information can be
 found through the IMAGE site: <http://image.llnl.gov>

Query W4: h 42 0% Score 12.6 E 17 Length 22
Best Local Similarity 60.0%, Field No. 4.6e-05,
Matches 18, Conservative 0, Mismatches 3, Indels 0, Gaps 0.

CY 3 AATTGGGCAAGACATTTTCTT 29
||||| ||| ||| ||| |||
1 AATTGGCTAATAACATTTTCTT 27

RESULT 7
PR92321/c 35 bp DNA Linear G2 02 Apr 2001
LOCUS PR92321/c
DEFINITION AAT118183 (A118183) TGA Insertion Site
Accession
VERSION
KEYWORDS
SOURCE
ORIGIN
Chale cress
Arabidopsis thaliana
Eukaryotic, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Euphyllophyta, Rosales, Fagales,
Rosaceae, Rosoideae, Rubi, Rosaceae, Rubus, Rubus
1 (bases 1 to 35)
Alonso, J.M., Lelso, T.J., Parajas, F., Chen, H., Chark, P., Gordinak,
C., Jeske, A., Karsch, M., Kim, C.J., Fawcett, H., Prentiss, L., Shih, F.,
Zimmerman, J., and Becker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Published 1999
Contact: Joseph R. Becker
Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 452 4100 x1952
Fax: 858 556 6370
Email: jbecker@salk.edu
This is single pass sequence recovered from the AAT118183
TGA. This sequence lies within an annotated exon of A118183.
Class: TGA 1999d
Location/Qualifiers

FEATURES
source
1..35
/organism="Arabidopsis thaliana"
/strain="Col-0"
/db_xref="taxon:3702"
/catalytic="GATC 33487-41323"
/catalytic="Arabidopsis thaliana TGA Insertion Site"
/catalytic="AAT118183 (A118183) TGA Insertion Site"
/catalytic="AAT118183 (A118183) TGA Insertion Site"
/catalytic="AAT118183 (A118183) TGA Insertion Site"
each of which contains two or more TGA insertion
elements. The resultant fragments for each site was
directly sequenced. A 4-bp site for primer extension
the site of insertion details of the fragments used can
be found at <http://catalytic.salk.edu/aat118183.html>

BASE COUNT
16 a 8 c 3 g 8 t
ORIGIN

Query W4: h 42 0% Score 12.6 E 17 Length 22
Best Local Similarity 78.9%, Field No. 4.6e-05,
Matches 15, Conservative 0, Mismatches 4, Indels 0, Gaps 0.

CY 12 AACAAATATTTTCTTCTT 30
||||| ||| ||| ||| |||
20 AACAAATATTTTCTTCTT 2

RESULT 8
AZ800963/c 37 bp DNA Linear G2 16 Feb 2001
LOCUS AZ800963/c
DEFINITION AAT118183 (A118183) TGA Insertion Site
Accession
VERSION
KEYWORDS
SOURCE
Chale cress
Arabidopsis thaliana
Eukaryotic, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Euphyllophyta, Rosales, Fagales,
Rosaceae, Rosoideae, Rubi, Rosaceae, Rubus, Rubus
1 (bases 1 to 37)
Alonso, J.M., Lelso, T.J., Parajas, F., Chen, H., Chark, P., Gordinak,
C., Jeske, A., Karsch, M., Kim, C.J., Fawcett, H., Prentiss, L., Shih, F.,
Zimmerman, J., and Becker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Published 1999
Contact: Joseph R. Becker
Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 452 4100 x1952
Fax: 858 556 6370
Email: jbecker@salk.edu
This is single pass sequence recovered from the AAT118183
TGA. This sequence lies within an annotated exon of A118183.
Class: TGA 1999d
Location/Qualifiers

ORIGIN
Mus musculus
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus,
1 (bases 1 to 27)
Dunn, D., Ayala, A., Barber, M., Beaton, T., Duval, R., Hant, C.,
Islam, H., Longcore, S., Mahmood, M., Meon, E., Pedersen, T., Pelly,
M., Rose, M., Rose, P., Stokes, R., Tinney, A., von Niederhausern, A.,
and Wright, D., Weiss, R.
Mouse whole-genome scaffolding with paired end reads from 198
Plasmid inserts
Published 2000
Contact: Robert E. Weiss
University of Utah Genome Center
Room 408, Biomedical Polymers Research Bldg., 20 S. 1400 E., Salt Lake
City, UT 84112, USA
Tel: 801 585 5406
Fax: 801 585 7177
Email: jbecker@salk.edu
Insert length: 19800 bp, Error: 0.00
Plate: 153, X: 1, Y: 2, Column: 16
Seq Project: GATC33487-41323
Class: plasmid ends
High quality sequence step: 27.
Location/Qualifiers

FEATURES
source
1..27
/organism="Mus musculus"
/strain="GSM/67"
/db_xref="taxon:10090"
/catalytic="GATC33487-41323"
/catalytic="GATC33487-41323"
/catalytic="GATC33487-41323"
/catalytic="GATC33487-41323"
each of which contains two or more TGA insertion
elements. The resultant fragments for each site was
directly sequenced. A 4-bp site for primer extension
the site of insertion details of the fragments used can
be found at <http://catalytic.salk.edu/aat118183.html>

BASE COUNT
5 a 5 c 7 g 10 t
ORIGIN

Query W4: h 42 0% Score 12.6 E 17 Length 27
Best Local Similarity 72.7%, Field No. 5.5e-05,
Matches 14, Conservative 0, Mismatches 6, Indels 0, Gaps 0.

CY 22 AATTGGGCAAGACATTTTCTT 24
||||| ||| ||| ||| |||
22 AATTGGGCAAGACATTTTCTT 1

RESULT 9
AZ807111 37 bp DNA Linear G2 16 Feb 2001
LOCUS AZ807111
DEFINITION AAT118183 (A118183) TGA Insertion Site
Accession
VERSION
KEYWORDS
SOURCE
Chale cress
Arabidopsis thaliana
Eukaryotic, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, Euphyllophyta, Rosales, Fagales,
Rosaceae, Rosoideae, Rubi, Rosaceae, Rubus, Rubus
1 (bases 1 to 37)
Alonso, J.M., Lelso, T.J., Parajas, F., Chen, H., Chark, P., Gordinak,
C., Jeske, A., Karsch, M., Kim, C.J., Fawcett, H., Prentiss, L., Shih, F.,
Zimmerman, J., and Becker, J.R.
A Sequence-Indexed Library of Insertion Mutations in the
Arabidopsis Genome
Published 1999
Contact: Joseph R. Becker
Salk Institute for Biological Studies
10010 N. Torrey Pines Road, La Jolla, CA 92037, USA
Tel: 858 452 4100 x1952
Fax: 858 556 6370
Email: jbecker@salk.edu
This is single pass sequence recovered from the AAT118183
TGA. This sequence lies within an annotated exon of A118183.
Class: TGA 1999d
Location/Qualifiers

[illegible]

[illegible]

TITLE OF INVENTION: HUMAN SINGLE NUCLEOTIDE POLYMORPHISMS
 FILE REFERENCE: 2009-009-001
 CURRENT APPLICATION NUMBER: 2009-009-001
 CURRENT FILING DATE: 2001-03-27
 PRIOR APPLICATION NUMBER: 18-457167-518
 PRIOR FILING DATE: 2000-06-07
 PRIOR APPLICATION NUMBER: 18-457167-518
 PRIOR FILING DATE: 2000-06-07
 NUMBER OF SEQ. ID NOS: 1402
 SOFTWARE: FASTEST 6.1 KLASIK Vast 1.4
 SEQ. ID NO: 1776
 LENGTH: 31
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-801-274-1778

Query Match: 43.3% Score 13, DB 13, Length 32
 Best Local Similarity: 57.1%, Field No. 21804
 Matches: 12, Conserved: 4, Mismatches: 5, Indels: 0, Gaps: 0

2 TAAATGGGAGAGAGATGTT 24
 9 TAAATGGGAGAGAGATGTT 21

RESULT 39
 US-09-230-926A-45
 Sequence 45: Application No. 2009-009-001
 Patent No. 2009-009-001
 GENERAL INFORMATION:
 APPLICANT: MARILYN, Claude
 APPLICANT: SCHLEIFER, Karl Heinz
 APPLICANT: LEWIS, Wolfgang
 TITLE OF INVENTION: NUCLEOTIDE SEQUENCE OF THE 230 RNA OF BACTERA OF THE GENUS CHAM
 TITLE OF INVENTION: USE AS A PROBE, PRIMER, AND IN A REAGENT AND A DETECTION METHOD
 FILE REFERENCE: 102662
 CURRENT APPLICATION NUMBER: 2009-009-001
 CURRENT FILING DATE: 1999-03-04
 PRIOR APPLICATION NUMBER: PCT/EP99/01157
 PRIOR FILING DATE: 1998-07-07
 PRIOR APPLICATION NUMBER: EP 37/01000
 PRIOR FILING DATE: 1997-06-05
 NUMBER OF SEQ. ID NOS: 60
 SOFTWARE: FASTEST 6.1 KLASIK Vast 1.4
 SEQ. ID NO: 45
 LENGTH: 32
 TYPE: RNA
 ORGANISM: Chlamydia psittaci
 US-09-230-926A-45

Query Match: 42.3% Score 13, DB 13, Length 32
 Best Local Similarity: 57.1%, Field No. 21804
 Matches: 12, Conserved: 4, Mismatches: 5, Indels: 0, Gaps: 0

2 TAAATGGGAGAGAGATGTT 22
 1 UCAATGGGAGAGAGATGTT 21

RESULT 40
 US-10-205-009-62
 Sequence 62: Application No. 2009-009-001
 Publication No. US20030114404A1
 GENERAL INFORMATION:
 APPLICANT: NEROUJA JANDIC, LARRY GIL, IAN G. SCHMIDT, CHANDRA
 APPLICANT: VARGHESE, MICHAEL WILLIS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NUCLEIC
 TITLE OF INVENTION: ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESS: Swanson and Rayburn, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200

CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIA TYPE: Diskette, 3.5 inch, 1.4 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT AFFILIATION DATA:
 AFFILIATION NUMBER: 2009-009-001
 FILING DATE: 25-JULY-2002
 CLASSIFICATION:
 APPLICATION NUMBER: 03/09/254,968
 FILING DATE: 13-MAR-2000
 APPLICATION NUMBER: 2009-009-001
 FILING DATE: 17-JULY-1997
 APPLICATION NUMBER: 02/32,102
 FILING DATE: 25-OCTOBER-1996
 APPLICATION NUMBER: 02/30,930
 FILING DATE: 6-JUNE-1997
 APPLICATION NUMBER: 08/097,351
 FILING DATE: 21-JULY-1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 TELECOMMUNICATIONS INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ. ID NOS: 62:
 SOURCE CHARACTERISTICS:
 LENGTH: 73
 TYPE: nucleic acid
 STRANDEDNESS: single
 MOLECULE TYPE: linear
 FEATURE:
 OTHER INFORMATION: All polymers are 5' flanked by
 OTHER INFORMATION: modified
 FEATURE:
 OTHER INFORMATION: C in position 23 is 2'-OH C
 US 10 205 009 62

Query Match: 42.3% Score 12.8, DB 13, Length 32
 Best Local Similarity: 57.1%, Field No. 38404
 Matches: 12, Conserved: 2, Mismatches: 2, Indels: 0, Gaps: 0

7 GGGGAGAGAGATG 22
 1 GGGGAGAGAGATG 10

Search completed: July 23, 2003, 18:30:03
 Job time: 89.6397 secs

```

CURRENT FILING DATE: 1997-12-15
PRIORITY APPLICATION NUMBER: US 60/084,459
PRIORITY FILING DATE: 1997-12-15
PRIORITY APPLICATION NUMBER: US 60/084,745
PRIORITY FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 16
LENGTH: 23
TYPE: DNA
ORGANISM: Rattus norvegicus
US-09-211 9230 16

```

```

Query Match 43.3% Score 13, DB 15, Length 25,
Best Local Similarity 76.2% Pred. No. 2,5e+04,
Matches 16, Conservative 0, Mismatches 5, Indels 0, gaps 0
Db 23 GCGACAGAAAGTGTCTCTCC 2

```

```

RESULT 34
US-10-098-263B-49911/c
Sequence 4911, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 49911
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B 49911

```

```

Query Match 43.3% Score 13, DB 15, Length 25,
Best Local Similarity 76.2% Pred. No. 2,5e+04,
Matches 16, Conservative 0, Mismatches 5, Indels 0, gaps 0
Db 21 TGTCACAAATAGAGTGTCTCC 1

```

```

RESULT 35
US-10-098-263B-49912/c
Sequence 4912, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 49912
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-49912

```

```

Query Match 43.3% Score 13, DB 15, Length 25,
Best Local Similarity 76.2% Pred. No. 2,5e+04,

```

```

Matches 16, Conservative 0, Mismatches 5, Indels 0, gaps 0
Query 6 TGTCACAAATAGAGTGTCTCC 26
Db 21 TGTCACAAATAGAGTGTCTCC 1

```

```

RESULT 36
US-10-098-263B-59654
Sequence 59654, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 59654
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B 59654

```

```

Query Match 43.3% Score 13, DB 15, Length 25,
Best Local Similarity 76.2% Pred. No. 2,5e+04,
Matches 16, Conservative 0, Mismatches 5, Indels 0, gaps 0
Query 10 GCGACAGAAAGTGTCTCTCC 30
Db 2 GTAAAGTGTCTCTCTCTCC 22

```

```

RESULT 37
US-10-098-263B-64031/c
Sequence 64031, Application US/10098263B
Publication No. US20030104410A1
GENERAL INFORMATION:
APPLICANT: Miltman, Michael
TITLE OF INVENTION: Human Microarray
FILE REFERENCE: 3118.1
CURRENT APPLICATION NUMBER: US/10/098,263B
CURRENT FILING DATE: 2003-01-08
PRIORITY APPLICATION NUMBER: 60/276,759
PRIORITY FILING DATE: 2001-03-16
NUMBER OF SEQ ID NOS: 131066
SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
SEQ ID NO 64031
LENGTH: 25
TYPE: DNA
ORGANISM: Homo sapien
US-10-098-263B-64031

```

```

Query Match 43.3% Score 13, DB 15, Length 25,
Best Local Similarity 76.2% Pred. No. 2,5e+04,
Matches 16, Conservative 0, Mismatches 5, Indels 0, gaps 0
Query 1 GTAAATGCGACAGAAATAT 21
Db 25 GTAAATGCGACAGAAATAT 5

```

```

RESULT 38
US-09-801-274-1778
Sequence 1778, Application US/09801274
Patent No. US6206042A1
GENERAL INFORMATION:
APPLICANT: Gargill, Michele
APPLICANT: Ireland, James S.
APPLICANT: Lander, Eric S.

```

NUMBER OF SEQ IN NO: 115000
 SOFTWARE: Microarray Probe Sequence Listing (v1.1)
 SEQ ID NO: 10603
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-890-363-12600

Query Match 44.0% Score 13.2; DB 15; Length 25;
 Best Local Similarity 81.3%; Pred. No. 2.1e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CV 12 AGAGAGATGTTCTGT 29
 DB 3 AGAGAGATGTTCTGT 20

RESULT 30
 US-09-890-363-12600
 Sequence 16, Application US/09030327A
 Publication No. US2002016433A1
 GENERAL INFORMATION:
 APPLICANT: HIRUMA, Shoichi
 APPLICANT: FUJIMOTO, Shoji
 TITLE OF INVENTION: NOVEL POLYMERIZABLE POLYMER AND ITS DNA
 FILE REFERENCE: 2000-0908
 CURRENT APPLICATION NUMBER: US/10/201,641
 PRIOR FILING DATE: 2000-09-08
 PRIOR APPLICATION NUMBER: US/00/010,000
 PRIOR FILING DATE: 2001-03-15
 PRIOR APPLICATION NUMBER: US/00/000,000
 PRIOR FILING DATE: 2000-02-17
 PRIOR APPLICATION NUMBER: US/00/000,000
 PRIOR FILING DATE: 2000-12-11
 NUMBER OF SEQ ID NOS: 3
 SEQ ID NO: 8
 LENGTH: 36
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Primer
 US-09-890-363-12600

Query Match 44.0% Score 13.2; DB 15; Length 39;
 Best Local Similarity 69.2%; Pred. No. 2.1e+04;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CV 2 TATTTCTTCAATATTTCTGT 27
 DB 1 TATTTCTTCAATATTTCTGT 26

RESULT 31
 US-09-890-363-12600
 Sequence 23, Application US/09030327A
 Patent No. US2002016433A1
 GENERAL INFORMATION:
 APPLICANT: NEMETZ, GREG E.
 APPLICANT: LI, BRUNY
 TITLE OF INVENTION: EFFICIENTLY NOVELLED AND VERIFIED COMBINED IMMUNITY FOR TUBER
 TITLE OF INVENTION: GENE
 TITLE OF INVENTION: SEQUENCE
 FILE REFERENCE: 2000-1208
 CURRENT APPLICATION NUMBER: US/09/030,327A
 CURRENT FILING DATE: 2001-07-10
 PRIOR APPLICATION NUMBER: US/01/013,111
 PRIOR FILING DATE: 2000-07-10
 NUMBER OF SEQ ID NOS: 33
 SOFTWARE: FASTSEQ for Windows Version 1.0
 SEQ ID NO: 23
 LENGTH: 39
 TYPE: DNA
 ORGANISM: Artificial Sequence

FEATURE:
 OTHER INFORMATION: PCR primer for cloning DAV-1 (right) chain for
 OTHER INFORMATION: amino acid sequence of DAV-1 constructs.
 US-09-890-363-12600

Query Match 44.0% Score 13.2; DB 15; Length 39;
 Best Local Similarity 81.3%; Pred. No. 2.1e+04;
 Matches 15; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

CV 13 AGAGAGATGTTCTGT 30
 DB 35 AGAGAGATGTTCTGT 18

RESULT 32
 US-09-737-379-16/c
 Sequence 16, Application US/070707070
 Patent No. US2007080702A1
 GENERAL INFORMATION:
 APPLICANT: BESSON, JEAN J.
 APPLICANT: BROOKS, DAVID
 APPLICANT: GILLAI, MERLOS
 APPLICANT: NELSON, STEPHAN
 APPLICANT: TANIGUCHI, MASASHI
 TITLE OF INVENTION: SCREENING METHOD USING DIAMETER OF THE
 TITLE OF INVENTION: NEUROFILAMENT PROTEIN H2A72
 FILE REFERENCE: AUS0037-1D1
 CURRENT APPLICATION NUMBER: US/07/070,707
 CURRENT FILING DATE: 2007-07-07
 PRIOR APPLICATION NUMBER: US/07/070,707
 PRIOR FILING DATE: 1997-09-26
 PRIOR APPLICATION NUMBER: US/07/070,707
 PRIOR FILING DATE: 1997-09-26
 PRIOR APPLICATION NUMBER: US/07/070,707
 PRIOR FILING DATE: 1997-07-02
 PRIOR APPLICATION NUMBER: US/07/070,707
 PRIOR FILING DATE: 1997-03-19
 PRIOR APPLICATION NUMBER: US/07/070,707
 PRIOR FILING DATE: 1997-12-17
 NUMBER OF SEQ ID NOS: 21
 SOFTWARE: FASTSEQ for Windows Version 3.0
 SEQ ID NO: 16
 LENGTH: 23
 TYPE: DNA
 ORGANISM: Rattus rattus
 US-09-737-379-16

Query Match 44.0% Score 13.2; DB 15; Length 23;
 Best Local Similarity 76.3%; Pred. No. 2.1e+04;
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CV 10 GAGAGAGATGTTCTGT 30
 DB 22 GAGAGAGATGTTCTGT 2

RESULT 33
 US-09-890-363-12600
 Sequence 16, Application US/09030327A
 Publication No. US2002016433A1
 GENERAL INFORMATION:
 APPLICANT: HIRUMA, Shoichi
 APPLICANT: FUJIMOTO, Shoji
 APPLICANT: LI, BRUNY
 APPLICANT: NEMETZ, GREG E.
 APPLICANT: PIPER, DAVID
 APPLICANT: SMITH, MARTIN J.
 APPLICANT: KENNETH, GUY ANTHONY
 APPLICANT: PATEL, SARASWATI R.
 TITLE OF INVENTION: METHOD OF TREATMENT USING COMBINED IMMUNITY
 TITLE OF INVENTION: OF THE NEUROFILAMENT RECEPTOR H2A72 AND ANTIBODIES
 TITLE OF INVENTION: ANTAGONISTS THEREOF
 FILE REFERENCE: P50745
 CURRENT APPLICATION NUMBER: US/09/030,327A

APPLICANT: 1st J. Caley
TITLE OF INVENTION: ALTERNATE PRIMER VECTORS
FILE REFERENCE: 0111-000002
CURRENT APPLICATION NUMBER: US/01/01/01/01
CURRENT FILING DATE: 2002-09-06
PRIOR APPLICATION NUMBER: 60/317,722
PRIOR FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 43
SOFTWARE: FASTSEQ for Windows Version 1.0
SEQ ID NO 43
LENGTH: 36
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-237-302-43

Query Match 44.7% Score 13.4 DB 12 Length 36
Best Local Similarity 93.9% Prog. No. 1.7e+04
Matches 14 Conserved 0 Mismatches 4 Indels 0 Gaps 0

QY 11 CAGAGCATGTTCTCT 30
DB 31 CAGAGCATGTTCTCT 12

RESULT 22
US-09-802-1108-125/G
Query Match 44.7% Score 13.4 DB 12 Length 36
Best Local Similarity 93.9% Prog. No. 1.7e+04
Matches 14 Conserved 0 Mismatches 4 Indels 0 Gaps 0

APPLICANT: Lacroix, Jean Michel
Dunn, James M.
Hull, May
TITLE OF INVENTION: METHOD, COMPOSITION AND IDENTIFICATION OF WITNESSING
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenahl & Larson LLP
STREET: PO Box 1068
CITY: Dillon
STATE: CO
COUNTRY: US
ZIP: 80435
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 Inch, 1.44 MB size 96
COMPILED: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/01/01/01
FILING DATE: 07 Mar 2001
CLASSIFICATION: 35100000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/01/01/01
FILING DATE: 07 Mar 2001
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Martha T.
REGISTRATION NUMBER: 30 039
REFERENCE TO OTHER APPLICATIONS:
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: (970) 468-6600
TELEFAX: (970) 468-0104
TELEX: <Unknown>
INFORMATION FOR CIP IN NO. 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

HYPOHETICAL: 10
APPLICANT: 10
FRAGMENT TYPE: Internal
SEQUENCE DESCRIPTION: SEQ ID NO: 125:
US-09-802-1108-125

Query Match 44.7% Score 13.4 DB 12 Length 36
Best Local Similarity 93.9% Prog. No. 1.7e+04
Matches 14 Conserved 0 Mismatches 4 Indels 0 Gaps 0

QY 13 AGAGCATGTTCTCT 27
DB 24 AGAGCATGTTCTCT 10

RESULT 23
US-10-098-2638-600/8/G
Query Match 44.7% Score 13.4 DB 15 Length 27
Best Local Similarity 93.9% Prog. No. 1.7e+04
Matches 14 Conserved 0 Mismatches 4 Indels 0 Gaps 0

APPLICANT: Maeda, Masatsugu
TITLE OF INVENTION: NOVEL HEMOGLOBIN REBEKOR PROTEIN, NP12
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenahl & Larson LLP
STREET: PO Box 1068
CITY: Dillon
STATE: CO
COUNTRY: US
ZIP: 80435
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 Inch, 1.44 MB size 96
COMPILED: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/05/930
FILING DATE: 07 Mar 2001
CLASSIFICATION: 35100000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/01/01/01
FILING DATE: 07 Mar 2001
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Martha T.
REGISTRATION NUMBER: 30 039
REFERENCE TO OTHER APPLICATIONS:
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: (970) 468-6600
TELEFAX: (970) 468-0104
TELEX: <Unknown>
INFORMATION FOR CIP IN NO. 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

Query Match 44.7% Score 13.4 DB 15 Length 27
Best Local Similarity 93.9% Prog. No. 1.7e+04
Matches 14 Conserved 0 Mismatches 4 Indels 0 Gaps 0

QY 14 CAGAGCATGTTCTCT 30
DB 24 CAGAGCATGTTCTCT 12

RESULT 24
US-10-105-930-11/C
Query Match 44.7% Score 13.4 DB 15 Length 27
Best Local Similarity 93.9% Prog. No. 1.7e+04
Matches 14 Conserved 0 Mismatches 4 Indels 0 Gaps 0

APPLICANT: Maeda, Masatsugu
TITLE OF INVENTION: NOVEL HEMOGLOBIN REBEKOR PROTEIN, NP12
NUMBER OF SEQUENCES: 189
CORRESPONDENCE ADDRESS:
ADDRESSEE: Oppenahl & Larson LLP
STREET: PO Box 1068
CITY: Dillon
STATE: CO
COUNTRY: US
ZIP: 80435
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette 3.5 Inch, 1.44 MB size 96
COMPILED: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/05/930
FILING DATE: 07 Mar 2001
CLASSIFICATION: 35100000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/01/01/01
FILING DATE: 07 Mar 2001
ATTORNEY/AGENT INFORMATION:
NAME: Larson, Martha T.
REGISTRATION NUMBER: 30 039
REFERENCE TO OTHER APPLICATIONS:
TELECOMMUNICATIONS INFORMATION:
TELEPHONE: (970) 468-6600
TELEFAX: (970) 468-0104
TELEX: <Unknown>
INFORMATION FOR CIP IN NO. 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid

? INFORMATION FOR SEQ ID NO: 90:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 29
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: RNA
 ? FEATURE:
 ? OTHER INFORMATION: All pyrimidines are 2' fluoro (2' F)
 ? OTHER INFORMATION: modified
 ? FEATURE:
 ? OTHER INFORMATION: Features are 2' OM (19) (2' OM) modified
 ? FEATURE:
 ? OTHER INFORMATION: A in position 10 and 22 is unmodified
 ? OTHER INFORMATION: (1.e., 2'-OH)
 ? US-10-205-009-80
 ?
 ? Query Match: 46.0%, Score 13.0, DP 15, Length 29,
 ? Best Local Similarity: 70.6%, Pctd. No. 1.2e+04,
 ? Mismatch: 12, Conservation: 2, Mismatch: 2, Indels: 0, Gaps: 1,
 ?
 ? 6 TGGCGAGAGAGATG 22
 ? |||||
 ? 6 UGCGGAGAGAGAUUG 22
 ?
 ? RESULT 15
 ? US-10-205-009-81
 ? Sequence 81, Application US/10205009
 ? Publication No. US20030114404A1
 ? GENERAL INFORMATION:
 ? APPLICANT: NEBCOJA CANITO, LARRY GOLD, FRED G. JENSEN, JAMES PA
 ? APPLICANT: VAKOBESE,
 ? APPLICANT: MICHAEL WILLIS
 ? TITLE OF INVENTION: VACCINAE ENVELOPIED WITH PA-128 (2' OM) NUCLEOTI
 ? TITLE OF INVENTION: ACID BINDING COMPLEXES
 ? NUMBER OF SEQUENCES: 139
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Swanson and Bratschun, L.L.C.
 ? STREET: 8400 East Prentice Avenue, Suite #200
 ? CITY: Denver
 ? STATE: Colorado
 ? COUNTRY: USA
 ? ZIP: 80111
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 ? COMPUTER: IBM compatible
 ? OPERATING SYSTEM: MS-DOS
 ? SOFTWARE: Word 7.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/254,968
 ? FILING DATE: 25-JULY-2002
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/254,968
 ? FILING DATE: 13-Mar-2000
 ? APPLICATION NUMBER: US/09/254,968
 ? FILING DATE: 13 OCTOBER 1997
 ? APPLICATION NUMBER: 08/735,109
 ? FILING DATE: 25 OCTOBER 1996
 ? APPLICATION NUMBER: 08/810,930
 ? FILING DATE: 6 JUNE 1997
 ? APPLICATION NUMBER: 08/897,351
 ? FILING DATE: 21 JULY 1997
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Barry J. Swanson
 ? REGISTRATION NUMBER: 25,215
 ? REFERENCE TO OTHER INFORMATION:
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (303) 793-3433
 ? TELEFAX: (303) 793-3433
 ? INFORMATION FOR SEQ ID NO: 81:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 30
 ? TYPE: nucleic acid

? LENGTH: 29
 ? TYPE: nucleic acid
 ? STRANDEDNESS: single
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: RNA
 ? FEATURE:
 ? OTHER INFORMATION: All pyrimidines are 2' fluoro (2' F)
 ? OTHER INFORMATION: modified
 ? FEATURE:
 ? OTHER INFORMATION: Features are 2' OM (19) (2' OM) modified
 ? FEATURE:
 ? OTHER INFORMATION: A in position 10 and G in position 11 are
 ? OTHER INFORMATION: unmodified (1.e., 2'-OH)
 ? US-10-205-009-81
 ?
 ? Query Match: 46.0%, Score 13.0, DP 15, Length 29,
 ? Best Local Similarity: 70.6%, Pctd. No. 1.2e+04,
 ? Mismatch: 12, Conservation: 2, Mismatch: 2, Indels: 0, Gaps: 1,
 ?
 ? 6 TGGCGAGAGAGATG 22
 ? |||||
 ? 6 UGCGGAGAGAGAUUG 22
 ?
 ? RESULT 16
 ? US-10-205-009-59
 ? Sequence 59, Application US/10205009
 ? Publication No. US20030114404A1
 ? GENERAL INFORMATION:
 ? APPLICANT: NEBCOJA CANITO, LARRY GOLD, FRED G. JENSEN, JAMES PA
 ? APPLICANT: VAKOBESE,
 ? APPLICANT: MICHAEL WILLIS
 ? TITLE OF INVENTION: VACCINAE ENVELOPIED WITH PA-128 (2' OM) NUCLEOTI
 ? TITLE OF INVENTION: ACID BINDING COMPLEXES
 ? NUMBER OF SEQUENCES: 139
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: Swanson and Bratschun, L.L.C.
 ? STREET: 8400 East Prentice Avenue, Suite #200
 ? CITY: Denver
 ? STATE: Colorado
 ? COUNTRY: USA
 ? ZIP: 80111
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 ? COMPUTER: IBM compatible
 ? OPERATING SYSTEM: MS-DOS
 ? SOFTWARE: Word 7.0
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/254,968
 ? FILING DATE: 25-JULY-2002
 ? CLASSIFICATION:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/254,968
 ? FILING DATE: 13 Mar 2000
 ? APPLICATION NUMBER: US/09/254,968
 ? FILING DATE: 13 OCTOBER 1997
 ? APPLICATION NUMBER: 08/735,109
 ? FILING DATE: 25 OCTOBER 1996
 ? APPLICATION NUMBER: 08/810,930
 ? FILING DATE: 6 JUNE 1997
 ? APPLICATION NUMBER: 08/897,351
 ? FILING DATE: 21 JULY 1997
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Barry J. Swanson
 ? REGISTRATION NUMBER: 25,215
 ? REFERENCE TO OTHER INFORMATION:
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (303) 793-3433
 ? TELEFAX: (303) 793-3433
 ? INFORMATION FOR SEQ ID NO: 59:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 30
 ? TYPE: nucleic acid

FILING DATE: 13 Mar 2000
APPLICATION NUMBER: PCT/US97/16944
FILING DATE: 17 October 1997
APPLICATION NUMBER: 08/739,109
FILING DATE: 25 October 1996
ATTORNEY/AGENT INFORMATION:
FILING DATE: 6 JUNE 1997
APPLICATION NUMBER: 08/897,351
FILING DATE: 21 JULY 1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/AGENT NUMBER: 08/897,351
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE: OTHER INFORMATION: All pyrimidines are 2'-fluoro 2'-F
OTHER INFORMATION: modified
US-10-205-009-60

Query Match 46.0% Score 13.8 DB 15 Length 28
Pct Local Similarity 70.0% Pct Global 10.0%
Matches 12 Conservative 3 Mismatches 2 Indels 0 Gaps 0

QY 6 TGGGCAAGAGATTG 22
|||||
DB 6 TGGGCAAGAGATTG 22

RESULT 11
US-10-205-009-61
Citation: 61, Application 02/1000003
Publication No. 020000144041
GENERAL INFORMATION:
APPLICANT: HERBERT LANTO, JERRY GOLD, PATT G SCHWARTZ, GRACEA
APPLICANT: VARGESE,
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR INHIBITORS
TITLE OF INVENTION: ACID LIPID COMPLEXES
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Frontview Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/897,351
FILING DATE: 25 OCTOBER 1996
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/897,351
FILING DATE: 13 MAR 2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/897,351
FILING DATE: 13 MAR 2000
APPLICATION NUMBER: 08/739,109
FILING DATE: 25 OCTOBER 1996
APPLICATION NUMBER: 08/739,109
FILING DATE: 6 JUNE 1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215

APPLICATION NUMBER: 08/897,351
FILING DATE: 21 JULY 1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/AGENT NUMBER: 08/897,351
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 61:
SEQUENCE CHARACTERISTICS:
LENGTH: 28
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE: OTHER INFORMATION: All pyrimidines are 2'-fluoro 2'-F
OTHER INFORMATION: modified
US-10-205-009-61

Query Match 46.0% Score 13.8 DB 15 Length 28
Pct Local Similarity 70.0% Pct Global 10.0%
Matches 12 Conservative 3 Mismatches 2 Indels 0 Gaps 0

QY 6 TGGGCAAGAGATTG 22
|||||
DB 6 TGGGCAAGAGATTG 21

RESULT 12
US-10-205-009-78
Citation: 78, Application 02/1000003
Publication No. 020000144041
GENERAL INFORMATION:
APPLICANT: HERBERT LANTO, JERRY GOLD, PATT G SCHWARTZ, GRACEA
APPLICANT: VARGESE,
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR INHIBITORS
TITLE OF INVENTION: ACID LIPID COMPLEXES
NUMBER OF SEQUENCES: 139
CORRESPONDENCE ADDRESS:
ADDRESSEE: Swanson and Bratschun, L.L.C.
STREET: 8400 East Frontview Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
COMPUTER: IBM compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/897,351
FILING DATE: 25 OCTOBER 1996
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/897,351
FILING DATE: 13 MAR 2000
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/897,351
FILING DATE: 13 MAR 2000
APPLICATION NUMBER: 08/739,109
FILING DATE: 25 OCTOBER 1996
APPLICATION NUMBER: 08/739,109
FILING DATE: 6 JUNE 1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry J. Swanson
REGISTRATION NUMBER: 33,215

OY 16 A0AMTCTTCTCT 22
 DB 7 A0AMTCTTCTCT 20

RESULT 4

US-10-116-288-16/c
 Sequence 16, Application US/01116288
 Publication No. US20020143142A1
 GENERAL INFORMATION
 APPLICANT: Lin, Yao Zhong
 APPLICANT: Donahue, John P.
 APPLICANT: Rojas, Mauricio
 APPLICANT: Tan, Zhongjia
 TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of Proteins with C-11 Membrane Translocating Activity"
 FILE REFERENCE: 2000-009703
 CURRENT APPLICATION NUMBER: US/0116-288
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: 03/044,853
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 06/186,170
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: 06/080,083
 PRIOR FILING DATE: 1998-03-31
 NUMBER OF SEQ ID NOS: 19
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 16
 LENGTH: 27
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
 OTHER INFORMATION: Sequence of the protein which translocates
 OTHER INFORMATION: Proteins through the cell membrane into the cell
 PUBLICATION INFORMATION:
 AUTHORS: Rojas, M. et al.
 TITLE: "Genetic Engineering of Proteins with Cell Membrane
 TITLE: Permeability"
 JOURNAL: Nature Biotechnology
 VOLUME: 16
 ISSUE: April
 PAGES: 370-375
 DATE: 1998-04-01
 US-10-116-288-17

Query Match 4678, Score 14, E-110, Long 100
 Best Local Similarity 100.0%, Freq No. 9,5e+03,
 Matches 14, Conservative 0, Mismatches 0, Indels 0, gaps 0

OY 6 TGGGCGAAGAGAA 19
 DB 24 TGGGCGAAGAGAA 11

RESULT 5

US-10-116-288-17/c
 Sequence 17, Application US/01116288
 Publication No. US20020143142A1
 GENERAL INFORMATION
 APPLICANT: Lin, Yao Zhong
 APPLICANT: Donahue, John P.
 APPLICANT: Rojas, Mauricio
 APPLICANT: Tan, Zhongjia
 TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of Proteins with C-11 Membrane Translocating Activity"
 FILE REFERENCE: 2000-009703
 CURRENT APPLICATION NUMBER: US/0116-288
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: 03/044,853
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 06/186,170
 PRIOR FILING DATE: 1998-11-04

PRIOR APPLICATION NUMBER: 60/080,083
 PRIOR FILING DATE: 1998-03-31
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 17
 LENGTH: 30
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
 OTHER INFORMATION: Sequence encoding protein which translocates
 OTHER INFORMATION: Proteins through the cell membrane into the cell
 PUBLICATION INFORMATION:
 AUTHORS: Rojas, M. et al.
 TITLE: "Genetic Engineering of Proteins with Cell Membrane
 TITLE: Permeability"
 JOURNAL: Nature Biotechnology
 VOLUME: 16
 ISSUE: April
 PAGES: 370-375
 DATE: 1998-04-01
 US-10-116-288-17

Query Match 4678, Score 14, E-110, Long 100
 Best Local Similarity 100.0%, Freq No. 9,5e+03,
 Matches 14, Conservative 0, Mismatches 0, Indels 0, gaps 0

OY 6 TGGGCGAAGAGAA 19
 DB 27 TGGGCGAAGAGAA 14

RESULT 6
 US-10-116-288-17/c
 Sequence 17, Application US/01116288
 Publication No. US20020143142A1
 GENERAL INFORMATION
 APPLICANT: Lin, Yao Zhong
 APPLICANT: Donahue, John P.
 APPLICANT: Rojas, Mauricio
 APPLICANT: Tan, Zhongjia
 TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of Proteins with C-11 Membrane Translocating Activity"
 FILE REFERENCE: 2000-009703
 CURRENT APPLICATION NUMBER: US/0116-288
 CURRENT FILING DATE: 2002-04-04
 PRIOR APPLICATION NUMBER: 03/044,853
 PRIOR FILING DATE: 2000-05-01
 PRIOR APPLICATION NUMBER: 06/186,170
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: 60/080,083
 PRIOR FILING DATE: 1998-03-31
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patent In Ver. 2.0
 SEQ ID NO: 14
 LENGTH: 33
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
 OTHER INFORMATION: Sequence encoding peptide which translocates
 OTHER INFORMATION: Proteins through the cell membrane into the cell
 PUBLICATION INFORMATION:
 AUTHORS: Rojas, M. et al.
 TITLE: "Genetic Engineering of Proteins with Cell Membrane
 TITLE: Permeability"
 JOURNAL: Nature Biotechnology
 VOLUME: 16
 ISSUE: April
 PAGES: 370-375
 DATE: 1998-04-01
 US-10-116-288-14

[illegible]

ALIGNMENTS

[illegible]

1 RESULT 1
 2 US 09-911-904-48/2
 3 Sequence ID: Affiliation US-09-911-904
 4 Publication No. us2003006234A1
 5 GENERAL INFORMATION
 6
 7 APPLICANT: Ficht, Spencer B.
 8 APPLICANT: Ficht, Gavin G.
 9 APPLICANT: Nelt, Robin Eileen
 10 APPLICANT: Durr, II, Robert Thomas
 11 TITLE OF INVENTION: CANINE TOXICITY GENES
 12 FILE REPRESENT: 41744-103-1
 13 CURRENT AFFILIATION NUMBER: 2002-04-09
 14 CURRENT FILING DATE: 2002-04-09
 15 PRIOR AFFILIATION NUMBER: 2002-04-09
 16 PRIOR FILING DATE: 2002-07-21
 17 NUMBER OF SEQ IN NO: 386
 18 SOFTWARE: FASTSEQ for Windows Version 4.0
 19 Seq. ID: 48
 20 LENGTH: 27
 21 TYPE: CDS
 22 ORGANISM: Canis familiaris
 23 US 09-911-904-48

Query Match	47/48	Score 14.5	SP 100	Length 27
Best Local Similarity	84.28%	Pred. No. 7.6e+03		
Matches 16, Conservative	0	Mismatches 3		Indels

2y 3 AATTGGGCAAGAGAAATT 2
 |||||
 3b 19 AATTGGGCAAGAGAAATT 1

RESULT

US-10-116-288-15/c
 Filed: 1998-04-01
 Publication No. 1998014912A1
 GENERAL INFORMATION:
 AFFILIANT: Lix, Yao Zhong
 APPLICANT: Donahue, John P.
 APPLICANT: Rojas, Mauricio
 APPLICANT: Tan, Zhongbia
 TITLE OF INVENTION: "Cell - and Tissue-based Methods for Genetic Engineering of Cells with Cell Membrane Translocation Activity"
 FILE REFERENCE: 2000-009703
 CURRENT AFFILIATION NUMBER: 01101117-288
 CURRENT FILING DATE: 2002-04-04
 P.R.P. APPLICATION NUMBER: 02/062,968
 PRIOR FILING DATE: 2000-05-01
 PRIOR AFFILIATION NUMBER: 00/186,170
 PRIOR FILING DATE: 1998-11-04
 PRIOR APPLICATION NUMBER: 00/000,083
 PRIOR FILING DATE: 1998-03-31
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: Patent Vsp 2.0
 SEQ ID NO 15
 LENGTH: 24
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthesized
 OTHER INFORMATION: Sequence encoding peptide which transports
 OTHER INFORMATION: Proteins through the cell membrane into the cell
 FUNCTIONAL INFORMATION:
 AUTHORS: Rojas, M. et al.
 TITLE: "Genetic Engineering of Proteins with Cell Membrane
 TITLE: "Permeability"
 JOURNAL: Nature Biotechnology
 VOLUME: 16
 ISSUE: April
 PAGES: 370-375
 DATE: 1998-04-01
 US-10-116-288-15/c

```

Query Match Similarity: 46.78; Score: 14; DB: 15; Length: 24
Best Local Similarity: 100.00; P-Val: 9.1e-03
Matches: 14; Conservative: 0; Mismatches: 0; Gaps: 0

```

RESULT 3
 SEQ ID NO 1: 122963
 INFORMATION: 10/17/2001 09:11:00 122963B
 PUBLICATION NO: US20030100410A1
 SERIAL INFORMATION:
 APPLICANT: Miltman, Michael
 TITLE OF INVENTION: Human Microarray
 FILE REFERENCE: 31181
 CURRENT APPLICATION NUMBER: US2001/001,753P
 CURRENT FILING DATE: 2003-01-08
 PRIORITY APPLICATION NUMBER: 09/272,476, 759
 PRIORITY FILING DATE: 2001-03-16
 NUMBER OF SEQ ID NOS: 13066
 SOFTWARE: Microarray Probe Sequence Listing
 Generated by: 1.1.1
 SEQ ID NO 122963
 LENGTH: 25
 TYPE: DNA
 ORGANISM: Homo Sapien
 15-10-098-263B-122963

Query Match	46.7%;	Score 14;	DB 15;	Length 25;
Best Local Similarity	100.0%;	Pred. No. 9.2e+03;		
Matches	14;	Conservative 0;	Mismatches 0;	Indels 0;



Db 1 TGCTACATCGAGATTCTTGCACT 24

RESULT 43
PCT-US95-07744A-19

Sequence 19, Application PCT/US9507744A

GENERAL INFORMATION:

APPLICANT: Trustees of The University of Pennsylvania

TITLE OF INVENTION: Plant Genes for Sensitivity to Ethylene

TITLE OF INVENTION: and Pathogens

NUMBER OF SEQUENCES: 82

CORRESPONDENCE ADDRESS:

ADDRESSEE: Woodcock, Macburn, Yurtz, MacLewison & Norris

STREET: One Liberty Place, 16th floor

CITY: Philadelphia

STATE: PA

COUNTRY: USA

ZIP: 19103

COMPUTER READABLE FORM:

MEDIA TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/07744A

FILING DATE: 15-JUNE-1995

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/251,822

FILING DATE: June 17, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Beardell, Lori Y.

REGISTRATION NUMBER: 34,293

TELEPHONE: (215) 568-4100

TELEFAX: (215) 568-3439

INFORMATION FOR SEQ ID NO: 19:

SEQUENCE CHARACTERISTICS:

LENGTH: 24 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYDROPHOBIC: NO

ANTI-SENSE: YES

PCT-US95-07744A-19

Query Match 42.7% Score 12.9; DB 5, Length 24;

Best Local Similarity 70.0%; Pval: No 3.5e+03;

Matches 17; Conservation 0; Mismatches 7; Indels 0; Gaps 0;

QY 6 TGGGAGAGAGATGTTCTGT 29

Db 1 TGCTACATCGAGATTCTTGCACT 24

Search completed: July 21, 2003, 15:48:47
Job time: 37.394 secs

NAME: Barry J Swanson
 REGISTRATION NUMBER: 13,215
 REFERENCE/DOCKET NUMBER: NEXUS/ECT US
 TELECOMMUNICATION INFORMATION
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 23:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE: OTHER INFORMATION: All pyrimidines are 2' fluoro (2'-F)
 modified
 FEATURE: OTHER INFORMATION: C in position 13 is 2' OH
 modified
 SEQUENCE ORIGIN: 5' to 3' direction
 US-09-254-968 62

Query Match 42.7% Score 12.8, E 4, Length 23,
 Best Local Similarity 75.0% (Seq No. 3,5e+03)
 Matches 12, Conservative 2, Mismatches 2, Indels 0, Gaps 0

QY 7 GCGGCAAGAAAGATTG 22
 |||||
 1 GCGGCAAGAAAGATTG 12

RESULT 39
 US-09-254-968-88
 Sequence 19, Application US/09241822A
 Patent No. 5650553
 GENERAL INFORMATION:
 APPLICANT: MFCOSA JANITY, LARRY GALT, RANDI SCHMIDT, CHANDRA VARGHESE,
 MICHAEL WILLIS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) NOBLEIG
 NUMBER OF SEQUENCES: 139
 CORRESPONDENT ADDRESS:
 ADDRESSEE: Swanson and Bratschan, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: CO 80231-4300
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 M, single
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/09241822A
 FILING DATE: 13 Mar 2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/09241822A
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 09/09241822A
 FILING DATE: 25 OCTOBER 1996
 APPLICATION NUMBER: 08/870,910
 FILING DATE: 6 JUNE 1997
 APPLICATION NUMBER: 08/897,351
 FILING DATE: 21 JULY 1997
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J Swanson
 REGISTRATION NUMBER: 13,215
 REFERENCE/DOCKET NUMBER: NEXUS/ECT US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433
 INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE: OTHER INFORMATION: All pyrimidines are 2' fluoro (2'-F)
 modified
 FEATURE: OTHER INFORMATION: Furios are 2' modified (2'-MO) modified
 FEATURE: OTHER INFORMATION: C in position 4 and A in position 6 are
 unmodified (1.0e+24-0H)
 SEQUENCE ORIGIN: 5' to 3' direction
 US-09-254-968-88

Query Match 42.7% Score 12.8, E 4, Length 23,
 Best Local Similarity 75.0% (Seq No. 3,5e+03)
 Matches 12, Conservative 2, Mismatches 2, Indels 0, Gaps 0

QY 7 GCGGCAAGAAAGATTG 22
 |||||
 1 GCGGCAAGAAAGATTG 16

RESULT 39
 US-09-254-968-19
 Sequence 19, Application US/09241822A
 Patent No. 5650553
 GENERAL INFORMATION:
 APPLICANT: Baker, Joseph R. et al.
 TITLE OF INVENTION: Fluorinated nucleosides and compositions
 NUMBER OF SEQUENCES: 82
 CORRESPONDENT ADDRESS:
 ADDRESSEE: Woodcock, Washburn, Kutz, Mankowski & N. J. J. J. J. J.
 STREET: One Liberty Place, 46th floor
 CITY: Philadelphia
 STATE: PA
 COUNTRY: USA
 ZIP: 19103
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/09241822A
 FILING DATE: 17 JUN 1994
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Beardsell, Lori Y.
 REGISTRATION NUMBER: 34,071
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (215) 568-3100
 TELEFAX: (215) 568-3439
 INFORMATION FOR SEQ ID NO: 19:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 24 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 HYPOTHETICAL: NO
 ANTI-SENSE: YES
 US-09-254-968-19

Query Match 42.7% Score 12.8, E 4, Length 24,
 Best Local Similarity 70.8% (Seq No. 3,5e+03)
 Matches 17, Conservative 2, Mismatches 7, Indels 0, Gaps 0

QY 6 TCGGCAAGAAAGATTGCT 29

Patent No. 616879
 GENERAL INFORMATION:
 APPLICANT: NERISSA JAMES, LARRY JILL, JAMES T. SWANSON, MICHAEL WILLIS
 TITLE OF INVENTION: VACCINE ENDOGENOUS GROWTH FACTOR (VEGF)
 TITLE OF INVENTION: NUCLEIC ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 98
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SWANSON AND BRATSCHEIN, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/08294968
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: C12
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 32,215
 REFERENCE/DOCKET NUMBER: 16061
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3333
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro
 FEATURE:
 OTHER INFORMATION: C in position 23 is 2'-OH
 US-09-870-930-58
 Query Match 42.7% Score 12.8, DB 4, Length 23
 Best Local Similarity 75.0% Freq No. 3.5e+03
 Mismatches 12, Conservations 2, Wildcards 2, Indels 2, Gaps 2
 QY 7 GCGGAAAGAAAGAAAG 22
 1 GCGGAAAGAAAGAAAG 16
 DB 1 GCGGAAAGAAAGAAAG 16
 RESULT 36
 US-09-870-930-94
 Sequence 84, Application US/08294968
 Patent No. 616879
 GENERAL INFORMATION:
 APPLICANT: NERISSA JAMES, LARRY JILL, JAMES T. SWANSON, MICHAEL WILLIS
 TITLE OF INVENTION: VACCINE ENDOGENOUS GROWTH FACTOR (VEGF)
 TITLE OF INVENTION: NUCLEIC ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 66
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschein, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08294968
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: C12
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 32,215
 REFERENCE/DOCKET NUMBER: 16061
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3333
 INFORMATION FOR SEQ ID NO: 84:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 23
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F) modified
 OTHER INFORMATION: 2'-fluoro are 2'-OH
 FEATURE:
 OTHER INFORMATION: 2'-fluoro, modified
 OTHER INFORMATION: 2'-fluoro, modified
 OTHER INFORMATION: In position 6 are unmodified (1,2,3, 2'-OH)
 US-09-870-930-94
 Query Match 42.7% Score 12.8, DB 4, Length 23
 Best Local Similarity 75.0% Freq No. 3.5e+03
 Mismatches 12, Conservations 2, Wildcards 2, Indels 2, Gaps 2
 QY 7 GCGGAAAGAAAGAAAG 22
 1 GCGGAAAGAAAGAAAG 16
 DB 1 GCGGAAAGAAAGAAAG 16
 RESULT 37
 US-09-254-568-62
 Sequence 84, Application US/08294968
 Patent No. 6426335
 GENERAL INFORMATION:
 APPLICANT: NERISSA JAMES, LARRY JILL, JAMES T. SWANSON, MICHAEL WILLIS
 TITLE OF INVENTION: VACCINE ENDOGENOUS GROWTH FACTOR (VEGF)
 TITLE OF INVENTION: ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschein, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS-DOS
 SOFTWARE: Word 7.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/07394968
 FILING DATE: 17 OCTOBER 1997
 APPLICATION NUMBER: 08/739,109
 FILING DATE: 25 OCTOBER 1996
 APPLICATION NUMBER: 08/870,930
 FILING DATE: 6 JUNE 1997
 APPLICATION NUMBER: 08/897,351
 FILING DATE: 21 JULY 1997
 ATTORNEY/AGENT INFORMATION:

FILING DATE: 04-AUG-1993
 INFORMATION FOR SEQ ID NO: 21:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 35 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MODREUCL TYPE: CUNA
 ORIGINAL SOURCE:
 ORGANISM: CWR112
 US 08-591 498-21

Query Match 44.3%, Score 15, E-03, Length 35,
 Best Local Similarity 76.2%, Fred. No. 3,1e-03,
 Matches 16; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CY 11 CAGAGAGATTGCTTC 26
 DB 20 CAGAGAGATTGCTTC 11

RESULT 33
 US-08-171-718-10/c
 Sequence 10, Application US/08171719
 Patent No. 5732863
 GENERAL INFORMATION:
 APPLICANT: Trolater, James A.
 APPLICANT: MacCollin, Mia M.
 APPLICANT: Gussella, James F.
 TITLE OF INVENTION: Tumor Suppressor Gene Mordin and Uses
 TITLE OF INVENTION: Therect
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/171,718
 FILING DATE: 22-DEC-1993
 CLASSIFICATION: 436
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/108,809
 FILING DATE: 19-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,054
 FILING DATE: 25-FEB-1993
 PRICE APPLICATION DATA:
 APPLICATION NUMBER: US 08/075,044
 FILING DATE: 04-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Anne
 REGISTRATION NUMBER: 36,463
 REFERENCE/DOCKET NUMBER: 0809,3850003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2500
 TELEFAX: (202) 371-2500
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US 08 171-718-10
 Query Match 42.7%, Score 12.8, E-03, Length 21,
 Sequence 58, Application US/08171719

Best Local Similarity 87.5%, Fred. No. 3.4e-03,
 Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 11 CAGAGAGATTGCTTC 26
 DB 20 CAGAGAGATTGCTTC 5

RESULT 34
 US-08-478-087-10/c
 Sequence 10, Application US/08478087
 Patent No. 6076585
 GENERAL INFORMATION:
 APPLICANT: Trolater, James A.
 APPLICANT: MacCollin, Mia M.
 APPLICANT: Gussella, James F.
 TITLE OF INVENTION: Tumor Suppressor Gene Mordin and Uses
 TITLE OF INVENTION: Therect
 NUMBER OF SEQUENCES: 120
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
 STREET: 1100 New York Avenue, N.W., Suite 600
 CITY: Washington
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005-3934
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC DOS/MS-DOS
 SOFTWARE: Patent Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/478,087
 FILING DATE: 07-JUN-1993
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/171,718
 FILING DATE: 22-DEC-1993
 APPLICATION NUMBER: US 08/108,808
 FILING DATE: 19-AUG-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/112,054
 FILING DATE: 25-FEB-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/075,044
 FILING DATE: 04-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Anne
 REGISTRATION NUMBER: 36,463
 REFERENCE/DOCKET NUMBER: 0809,3850003
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (202) 371-2500
 TELEFAX: (202) 371-2500
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 21 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 US-08-478-087-10
 Query Match 42.7%, Score 12.8, E-03, Length 21,
 Sequence 58, Application US/08478087

PRIOR APPLICATION DATA:
PILING DATE: 26 SEPT 1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER: GB/89/094
PILING DATE: 2 JUL 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB/92B/512
PILING DATE: 19 MAR 1997
APPLICATION NUMBER: GB/93/604
PILING DATE: 17 DEC 1997
AGENT INFORMATION:
NAME: KING, William T.
REGISTRATION NUMBER: 30954
REFERENCE TO SET NUMBER: ATC/009/-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610 270 5219
TELEX: 610 270 4016

SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA

US-GB 939-093A-16

Query March 43.3% Score 13; DB 4; Length 21;
Date Dec 1997 Word 16; Pct. Id. 43.3%;
Matches 10; Conserved 0; Mismatches 5; Indels 0

CY 19 GCAGACGAAATGGTTCCTGC 30
+|||||++++|||++
PB 22 GGTCAAGAGCGTGTTCTCCG 2

RESULT 32
Seq-id: 22; Accession: U00000.1;28
Patent No. 573694
GENERAL INFORMATION:
APPLICANT: BROCKHART, WILLEM F.
APPLICANT: CAMKUE, BRUNO P.A.
APPLICANT: REES, SARAH B.
TITLE OF INVENTION: ANTIMICROBIAL PROTEINS
NMP# OF SPINDERS: 25
CORRESPONDENCE ADDRESS:
ADDRESSER: CUSHMAN DABBY & COHRMAN
ADDRESSER: TELLSBOROUGH TRADING LTD
ADDRESSER: TELLSBOROUGH MADISON & SUTRO LLP
CINERY: 1100 New York Avenue, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/Ms DOS
SOFTWARE: Patent Release #1.0, Version #1.05
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,458
PILING DATE: 25 JAN 1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PT/GB94/01636
PILING DATE: 29 JUN 1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 937616.8
PILING DATE: 2/AUG-1993
PRIOR APPLICATION DATA: GB 9416198.6

1 TITLE OF INVENTION: 1ecches.
2 NUMBER OF SEQUENCES: 23
3 CORRESPONDING AUTHOR:
4 ADDRESS:R. Koll & Weinkauff
5 STREET: 1101 Connecticut Avenue
6 CITY: Washington
7 STATE: D.C.
8 COUNTRY: USA
9 ZIP: 20036
10
11 COMPUTER READABLE FORM:
12 MEDIUM TYPE: Diskette, 5.25 inch, 360 KB storage
13 COMPUTER: IBM AT-compatible, 80486 processor
14 OPERATING SYSTEM: MS-DOS version 5.0
15 SOFTWARE: WordPerfect version 5.1
16 CURRENT APPLICATION DATA
17 APPLICATION NUMBER: US/08/244,113
18
19 FILING DATE:
20 CLASSIFICATION: G36
21 CLASSIFICATION: C67K 73/10
22 CLASSIFICATION: A61K 37/64
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: PCT/EP92/02661
25 FILING DATE: 19-NOV-1992
26
27 INFORMATION FOR SEQ. 13 NO: 14:
28 SEQUENCE CHARACTERISTICS:
29 LENGTH: 23 base pairs
30 TYPE: nucleic acid
31 STRANDEDNESS: single
32 TOPOLOGY: linear
33
34 US:08 244-113 14

09 1 *****
Db 2 G*****
RESULT 28
US-09 311-260 125/c
Patent No. 621455
GENERAL INFORMATION:
APPLICANT: Leachman, James
APPLICANT: Hull, May
APPLICANT: Dunn, James M.
APPLICANT: Lacyoix, Jean-Michel
TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF POLYMER FILMS
TITLE OF INVENTION: POLYMERS
NUMBER OF SECTIONS: 144
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Oppehl & Lauson LLP
STREET: P.O. Box 5270
CITY: FRISCO
STATE: CO
COUNTRY: US
ZIP: 80441-5270
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 144 MB, single-sided
COMPUTER: IBM compatible
OPERATING SYSTEM: MS DOS
SOFTWARE: Word Perfect
CURRENT AFFILIATION DATA:
APPLICATION NUMBER: us/09/311,260
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:

NAME: Larson, Marina T.
REGISTRATION NUMBER: 27,038
FEES: \$1000.00
TELECOMMUNICATION INFORMATION:
TELEPHONE: (970) 668-2060
TELEFAX: (970) 668-2082
TELEX:
INFORMATION FOR SEQ ID NO: 125:
SEQUENCE CHARACTERISTICS:
LENGTH: 25
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHEetical: no
ANTI SENSE: no
FRAGMENT TYPE: internal
LOCUS: 27,038-125

Every Match	44 78	Score 13.4	Dr 4	Length 20
Best Local Similarity	93.3%	Pred. No. 1.9(+0.3)		
Matches 14	Conservative 6	Mismatches 11	Total 17	Gap 0
13 AATAAATGCTCT	27			
24 AGAAGCATGTTCT	10			

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07      13 AAAAAATTGTTCT 27
        ||||| |||||||
Db      24 AGAAGCATGTTCCT 10

RESULT 29
US-09-484-617-43
US-09-484-617-43 Affiliation US/09484617
Sequence 43, Affiliation US/09484617
Patent No. 6303374
GENERAL INFORMATION:
APPLICANT: Alex M. Cowsett
APPLICANT: Hertz Chair
TIME OF INVENTION: ANTISENSE MEDIATION OF CASPASE - EXPRESSION
FILE REFERENCE: RTS-0103
CURRENT APPLICATION NUMBER: US/09484,617
CURRENT FILING DATE: 2000 01 18
NUMBER OF SEQ ID NOS: 176
SEQ ID NO 43
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense oligonucleotide
US-09-484-617-43

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Query Match 44 01: Score 13 21 IP 41 Length 201
Post Local Similarity 44 01: 13 21 41 201
Matches 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836

17 1 11111111111111111111 20
 18 1 11111111111111111111 11
 19 3 11111111111111111111 20
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REFERENCE/DOCKET NUMBER: NEXA1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 5'-fluoro
FEATURE:
OTHER INFORMATION: N at position 30 is a 4'-3' linked
OTHER INFORMATION: 3'-3' linked deoxythymidine
US-09-870-930-55

Query Match: 46.0%, Score 13.8, Pos 4, Length 30
Best local similarity: 70.6%, Pos 1,3e+03
Matches: 10, Conservative: 3, Mismatches: 2, Indels: 0, Gaps: 0

CY 6 TGGGCAAGAGATG 22
EE :|||||:|||||:
6 US-09-870-930-55

RESULT 25
US-09-254-968-59
Sequence 59, Application US/0924968
Patent No. 642632
GENERAL INFORMATION:
APPLICANT: NEMESA SMITH, DAVID LEE, JAMES L. CHAMPA VAN HEELE,
MICHAEL WILLIS
TITLE OF INVENTION: SYSTEMS FOR THE DETECTION OF NUCLEIC ACID SEQUENCES
NUMBER OF SEQUENCES: 1
REFERENCE ADDRESS:
ADDRESSER: Swanson and Proctor, P.C.
STREET: 8400 East Prentice Avenue, Suite #200
CITY: Denver
STATE: Colorado
COUNTRY: USA
ZIP: 80111
COMPUTER READABLE FORM:
MEDIUM TYPE: Magnetic, 3 1/2 inch, 14 MB storage
COMMENTS: IBM compatible
(C) OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/254,968
FILING DATE: 13-Mar-2000
CLASSIFICATION: Unknown
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/114,411
FILING DATE: 13-October-1997
APPLICATION NUMBER: US/09/114,411
FILING DATE: 25-October-1996
APPLICATION NUMBER: US/09/114,411
FILING DATE: 6-June-1997
APPLICATION NUMBER: US/09/114,411
FILING DATE: 21-July-1997
ATTORNEY/AGENT INFORMATION:
NAME: Barry D. Swanson
REGISTRATION NUMBER: 33,215
REFERENCE/DOCKET NUMBER: NEXA1/968-59
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 793-3333
TELEFAX: (303) 793-3433
INFORMATION FOR SEQ ID NO: 59:
SEQUENCE CHARACTERISTICS:
LENGTH: 30
TYPE: nucleic acid

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```

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: RNA
FEATURE:
OTHER INFORMATION: All pyrimidines are 2'-fluoro
FEATURE:
OTHER INFORMATION: N at position 30 is a 4'-3' linked
OTHER INFORMATION: 3'-3' linked deoxythymidine
US-09-254-968-59

Query Match: 46.0%, Score 13.8, Pos 4, Length 30
Best local similarity: 70.6%, Pos 1,3e+03
Matches: 10, Conservative: 3, Mismatches: 2, Indels: 0, Gaps: 0

CY 6 TGGGCAAGAGATG 22
EE :|||||:|||||:
6 US-09-254-968-59

RESULT 26
US-09-540-014-8/C
Sequence 8, Application US/09540014
Patent No. 6980372
GENERAL INFORMATION:
APPLICANT: Cho, Myoung-Je
APPLICANT: Del Val, Greg
APPLICANT: Caliau, Maxime
APPLICANT: Lemaitre, Peggy G.
APPLICANT: Buchanan, Bob B.
TITLE OF INVENTION: Battery Gene for Mitochondria and
TITLE OF INVENTION: Nucleic Acid Sequences and
FILE REFERENCE: 2001-070130
CURRENT APPLICATION NUMBER: US/09/540,014
PRIOR APPLICATION NUMBER: US/00/031,198
PRIOR FILING DATE: 1999-03-31
PRIOR APPLICATION NUMBER: US/00/031,162
PRIOR FILING DATE: 1999-12-06
PRIOR APPLICATION NUMBER: US/00/177,740
PRIOR FILING DATE: 2000-01-21
PRIOR APPLICATION NUMBER: US/00/177,739
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 51
SOFTWARE: FASTCH for Windows Version 4.0
SEQ ID NO: 8
LENGTH: 34
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Primer
US-09-540-014-8

Query Match: 46.0%, Score 13.8, Pos 4, Length 34
Best local similarity: 70.6%, Pos 1,3e+03
Matches: 10, Conservative: 3, Mismatches: 2, Indels: 0, Gaps: 0

CY 34 ATTGGGCAAGAGATG 28
EE :|||||:|||||:
34 US-09-540-014-8

RESULT 27
US-09-244-113-14
Sequence 14, Application US/09244113
Patent No. 5456181
GENERAL INFORMATION:
APPLICANT: Strube, Karl-Hermann
APPLICANT: Bialojan, Siegfried
APPLICANT: Kriesger, Burkard
APPLICANT: Friedrich, Thomas
TITLE OF INVENTION: NO. 5456181: Chromatin-antibody

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(C) OPERATING SYSTEM: MS-DOS
SOFTWARE: Word 7.0
CURRENT APPLICATION DATA:
  AFFILIATION NUMBER: 127733/1894
  FILING DATE: 13 Mar 1999
  CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPL. FILE NUMBER: 127733/18944
  FILING DATE: 17 October 1997
  APPLICATION NUMBER: 28733/109
  FILING DATE: 25 October 1996
  APPLICATION NUMBER: 28733/109
  FILING DATE: 6 June 1997
  APPLICATION NUMBER: 28733/109
  FILING DATE: 21 July 1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Barry J. Swanson
    REGISTRATION NUMBER: 337215
    REFERENCE/DESCRIPT NUMBER: NLX157411 US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (303) 793-3333
    TELEFAX: (303) 793-3333
  INFORMATION FOR SEQ ID NO: 80:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 29
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: RNA
    FEATURE:
      modified
    OTHER INFORMATION: All pyrimidines are 2' fluoro (2'-F)
  FEATURE:
    OTHER INFORMATION: Purines are 2'-O-methyl (2'-OMe) modified
  OTHER INFORMATION: 3 in positions 10 and 22 is unmodified
  (10, 27 OH)
  SEQUENCE DESCRIPTION: SEQ ID NO: 80:
  46 08 5000 13 9 15 4 Length 29
  Best local similarity 70.6% Pred. No. 1.3e+03
  Matches 12, conservative 3, Mismatches 0, Indels 0, Gaps 0
  Query Match
  46 08 5000 13 9 15 4 Length 29
  Best local similarity 70.6% Pred. No. 1.3e+03
  Matches 12, conservative 3, Mismatches 0, Indels 0, Gaps 0
  RESULT 23
  US-09-254-968-81
  Sequence 81, Application us-09-254-968-81
  Patent No. 6168778
  GENERAL INFORMATION:
  APPLICANT: NELOUSA JANDIG, LARRY GOLD, JAVD G. SCHMITT, CHARNEA VANBERNE, MICHAEL
  TITLE OF INVENTION: VASCULAR ENDOGENOUS GROWTH FACTOR (VEGF) INHIBIT
  NUMBER OF SEQUENCES: 118
  ADDRESSSEE: Swanson and Bratschun, Ltd.
  CITY: Denver
  STATE: Colorado
  COUNTRY: USA
  ZIP: 80111
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
  COMPUTER: IBM compatible
  OPERATING SYSTEM: MS-DOS
  SOFTWARE: Word 7.0
  CURRENT APPLICATION DATA:
  AFFILIATION NUMBER: 127733/1894

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FILING DATE: 13-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
  APPL. FILE NUMBER: 127733/18944
  FILING DATE: 17 October 1997
  APPLICATION NUMBER: 28733/109
  FILING DATE: 25 October 1996
  APPLICATION NUMBER: 28733/109
  FILING DATE: 6 June 1997
  APPLICATION NUMBER: 28733/109
  FILING DATE: 21 July 1997
  ATTORNEY/AGENT INFORMATION:
    NAME: Barry J. Swanson
    REGISTRATION NUMBER: 337215
    REFERENCE/DESCRIPT NUMBER: NLX157411 US
  TELECOMMUNICATION INFORMATION:
    TELEPHONE: (303) 793-3333
    TELEFAX: (303) 793-3333
  INFORMATION FOR SEQ ID NO: 81:
    SEQUENCE CHARACTERISTICS:
      LENGTH: 29
      TYPE: nucleic acid
      STRANDEDNESS: single
      TOPOLOGY: linear
    MOLECULE TYPE: RNA
    FEATURE:
      modified
    OTHER INFORMATION: All pyrimidines are 2' fluoro (2'-F)
  FEATURE:
    OTHER INFORMATION: Purines are 2'-O-methyl (2'-OMe) modified
  OTHER INFORMATION: 3 in positions 10 and 22 is unmodified
  (10, 27 OH)
  SEQUENCE DESCRIPTION: SEQ ID NO: 81:
  46 08 5000 13 9 15 4 Length 29
  Best local similarity 70.6% Pred. No. 1.3e+03
  Matches 12, conservative 3, Mismatches 2, Indels 0, Gaps 0
  Query Match
  46 08 5000 13 9 15 4 Length 29
  Best local similarity 70.6% Pred. No. 1.3e+03
  Matches 12, conservative 3, Mismatches 2, Indels 0, Gaps 0
  RESULT 24
  US-09-870-930-55
  Sequence 55, Application us-09-870-930-55
  Patent No. 6168778
  GENERAL INFORMATION:
  APPLICANT: NELOUSA JANDIG, LARRY GOLD, JAVD G. SCHMITT, CHARNEA VANBERNE, MICHAEL
  TITLE OF INVENTION: VASCULAR ENDOGENOUS GROWTH FACTOR (VEGF) INHIBIT
  NUMBER OF SEQUENCES: 88
  ADDRESSSEE: Swanson and Bratschun, Ltd.
  CITY: Denver
  STATE: Colorado
  COUNTRY: USA
  ZIP: 80111
  COMPUTER READABLE FORM:
  MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
  COMPUTER: IBM compatible
  OPERATING SYSTEM: MS-DOS
  SOFTWARE: WordPerfect 8.0
  CURRENT APPLICATION DATA:
  APPL. FILE NUMBER: US/09/870-930
  FILING DATE: 6 JUNE 1997
  CLASSIFICATION: 536
  ATTORNEY/AGENT INFORMATION:
    NAME: Barry J. Swanson
    REGISTRATION NUMBER: 337215

```

STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 13-Mar-2000
 CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 13-Mar-1997
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 25-October-1996
 APPLICATION NUMBER: 08/09/1996
 FILING DATE: 6-June-1997
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 21-July-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Barry D. Swanson
 REGISTRATION NUMBER: 33,215
 FILING JURISDICTION: NEW YORK, NY
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433

INFORMATION FOR PUBLICATION:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA

FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
 modified

FEATURE:
 OTHER INFORMATION: Features are 2' (methoxy) (2'-OMe) modified

FEATURE:
 OTHER INFORMATION: G in position 10 and A in position 12 and G in position 22 are unmodified (1-P, 2'-OH)

SEQUENCE DESCRIPTION: SEQ ID NO: 781
 US-09-254 960 70

C-177 Match 46.0% Score 13.87 DR 4; Length 19;
 Best Local Similarity 70.63; Pred. No. 1.3e+03;
 Matches 12; Conservative 3; Mismatches 2; Inbels 0; Gaps 0

6 TGGCGAAGAGAAATG 22
 :|||||
 6 UCGGUGAGAGAAATG 22

RESULT 21
 US-09-254 960 70
 Sequence 73, Affiliation 08/09/1996
 Patent No. 6426335

GENERAL INFORMATION:
 APPLICANT: HERBERT JACOB, LARRY JOEL, PAUL J. SWANSON, CHARITA WATERS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INHIBITORS
 ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Ratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible
 (C) OPERATING SYSTEM: MS-DOS

SOFTWARE: Word 7.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 13-Mar-2000
 CLASSIFICATION: UNKNOWN

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 17-October-1997
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 25-October-1996
 APPLICATION NUMBER: 08/09/1996
 FILING DATE: 6-June-1997
 APPLICATION NUMBER: 08/09/1997
 FILING DATE: 21-July-1997

ATTORNEY/AGENT INFORMATION:
 NAME: Barry D. Swanson
 REGISTRATION NUMBER: 33,215
 FILING JURISDICTION: NEW YORK, NY
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-3433

INFORMATION FOR PUBLICATION:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 29
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA

FEATURE:
 OTHER INFORMATION: All pyrimidines are 2'-fluoro (2'-F)
 modified

FEATURE:
 OTHER INFORMATION: Features are 2' (methoxy) (2'-OMe) modified

FEATURE:
 OTHER INFORMATION: G in position 10 and A in position 12 are unmodified (1-P, 2'-OH)

SEQUENCE DESCRIPTION: SEQ ID NO: 781
 US-09-254 960 70

C-177 Match 46.0% Score 13.87 DR 4; Length 19;
 Best Local Similarity 70.63; Pred. No. 1.3e+03;
 Matches 12; Conservative 3; Mismatches 2; Inbels 0; Gaps 0

6 TGGCGAAGAGAAATG 22
 :|||||
 6 UCGGUGAGAGAAATG 22

RESULT 22
 US-09-254-968-80
 Sequence 73, Affiliation 08/09/1996
 Patent No. 6426335

GENERAL INFORMATION:
 APPLICANT: HERBERT JACOB, LARRY JOEL, PAUL J. SWANSON, CHARITA WATERS
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF) INHIBITORS
 ACID LIGAND COMPLEXES
 NUMBER OF SEQUENCES: 139
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Ratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage
 COMPUTER: IBM compatible

OTHER INFORMATION: All pyrimidines are 2'-fluoro
 FEATURE:
 OTHER INFORMATION: Purines are 2'-O-methyl
 OTHER INFORMATION: (2'-OMe) modified
 FEATURE:
 OTHER INFORMATION: G in position 10 and A in
 OTHER INFORMATION: position 12 are unmodified (i.e., 2'-OH)
 US-09-870-930-75

Query Match 46.0% Score 13.8 DB 4 Length 29
 Best Local Similarity 70.6% Pred No 1 3a-0%
 Matches 12 Conservative 3 Mismatches 2 Inbds 0 Gaps 0

DB 6 TCCGACAGCAATG 22
 6 TCCGACAGCAATG 22

RESULT 18

US-09-870-930-75
 Sequence 76, Application US/09870930
 Patent No. 6168778

GENERAL INFORMATION
 APPLICANT: NEBOJSA JANDIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VASARESE, MICHAEL
 TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)
 TITLE OF INVENTION: VEGF-A10 LIGAND ANALOGUES
 NUMBER OF SEQUENCES: 88
 CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 8400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS DOS

SOFTWARE: Mithras 9.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09-870-930-75

FILING DATE: 6 JUNE 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX91

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

OTHER INFORMATION: A in position 12 and G

OTHER INFORMATION: 16 position 22 are unmodified (i.e., 2'-OH)

SEQUENCE CHARACTERISTICS:

LENGTH: 29

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2'-fluoro

OTHER INFORMATION: Purines are 2'-O-methyl

OTHER INFORMATION: (2'-OMe) modified

FEATURE:

OTHER INFORMATION: G in position 12 and A in

OTHER INFORMATION: position 22 are unmodified (i.e., 2'-OH)

US-09-870-930-75

Query Match 46.0% Score 13.8 DB 4 Length 29

Best Local Similarity 70.6% Pred No 1 3a-0%

Matches 12 Conservative 3 Mismatches 2 Inbds 0 Gaps 0

DB 6 TCCGACAGCAATG 22

DB 6 TCCGACAGCAATG 22

RESULT 19

US-09-870-930-75

Sequence 77, Application US/09870930

Patent No. 6168778

GENERAL INFORMATION:

APPLICANT: NEBOJSA JANDIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VASARESE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

TITLE OF INVENTION: VEGF-A10 LIGAND ANALOGUES

NUMBER OF SEQUENCES: 88

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.

STREET: 8400 East Prentice Avenue, Suite #200

CITY: Denver

STATE: Colorado

COUNTRY: USA

ZIP: 80111

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.4 Mb storage

COMPUTER: IBM compatible

OPERATING SYSTEM: MS-DOS

SOFTWARE: Mithras 9.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09-870-930-75

FILING DATE: 6 JUNE 1997

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Barry J. Swanson

REGISTRATION NUMBER: 33,215

REFERENCE/DOCKET NUMBER: NEX91

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 793-3433

TELEFAX: (303) 793-3433

OTHER INFORMATION: A in position 12 and G

OTHER INFORMATION: 16 position 22 are unmodified (i.e., 2'-OH)

SEQUENCE CHARACTERISTICS:

LENGTH: 29

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: RNA

FEATURE:

OTHER INFORMATION: All pyrimidines are 2'-fluoro

OTHER INFORMATION: Purines are 2'-O-methyl

OTHER INFORMATION: (2'-OMe) modified

FEATURE:

OTHER INFORMATION: A in position 12 and G

OTHER INFORMATION: 16 position 22 are unmodified (i.e., 2'-OH)

US-09-870-930-75

Query Match 46.0% Score 13.8 DB 4 Length 29

Best Local Similarity 70.6% Pred No 1 3a-0%

Matches 12 Conservative 3 Mismatches 2 Inbds 0 Gaps 0

DB 6 TCCGACAGCAATG 22

6 TCCGACAGCAATG 22

RESULT 20

US-09-254-968-78

Sequence 76, Application US/09254968

Patent No. 6426315

GENERAL INFORMATION:

APPLICANT: NEBOJSA JANDIC, LARRY GOLD, PAUL G. SCHMIDT, CHANDRA VASARESE, MICHAEL

TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR (VEGF)

TITLE OF INVENTION: VEGF-A10 LIGAND ANALOGUES

NUMBER OF SEQUENCES: 119

CORRESPONDENCE ADDRESS:

ADDRESSEE: Swanson and Bratschun, L.L.C.

QY 6 TCGGCGACAGAGAA 19
 DB 30 TCGGCGACAGAGAA 17

RESULT 10

US-09-562-868-14/C
 Sequence ID: 14, Alignment: 100.00, Score: 46.78
 Patent No. 6432680
 GENERAL INFORMATION:
 APPLICANT: Lian, Yao Zhong
 APPLICANT: Donahue, John P.
 APPLICANT: Rojas, Mauricio
 APPLICANT: Tan, Zhongjia
 TITLE OF INVENTION: "Sequences and Methods for Genetic Engineering of
 Patent No. 6432680
 TITLE OF INVENTION: "Sequences and Methods for Genetic Engineering of
 FILING REFERENCE: 2000 060702 02/04/02, seq
 CURRENT FILING DATE: 2000 06-01
 PRIOR APPLICATION NUMBER: 60/360,083
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 09/166,170
 PRIOR FILING DATE: 1998-11-04
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 14
 LENGTH: 33
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
 OTHER INFORMATION: Sequence submitted with "14" and "15"
 OTHER INFORMATION: Proteins through the cell membrane into the cell
 PUBLICATION INFORMATION:
 AUTHORS: Rojas, M. et al.
 TITLE: "Genetic Engineering of Proteins with Cell Membrane
 TITLE: Permeability"
 JOURNAL: Nature Biotechnology
 VOLUME: 16
 ISSUE: April
 PAGES: 370-375
 DATE: 1998-04-01
 US-09-562-868-14

Query Match 46.78 Score 14, DB 4, Length 33
 Best Local Similarity: 100.00, Pct ID: 100.00
 Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

QY 6 TCGGCGACAGAGAA 19
 DB 30 TCGGCGACAGAGAA 20

RESULT 11

US-09-562-868-18/C
 Sequence ID: 18, Alignment: 100.00, Score: 46.78
 Patent No. 6432680
 GENERAL INFORMATION:
 APPLICANT: Lian, Yao Zhong
 APPLICANT: Donahue, John P.
 APPLICANT: Rojas, Mauricio
 APPLICANT: Tan, Zhongjia
 TITLE OF INVENTION: "Sequences and Methods for Genetic Engineering of
 Patent No. 6432680
 TITLE OF INVENTION: "Sequences and Methods for Genetic Engineering of
 FILING REFERENCE: 2000 060702 02/04/02, seq
 CURRENT FILING DATE: 2000 06-01
 PRIOR APPLICATION NUMBER: 60/360,083
 PRIOR FILING DATE: 1998-03-31
 PRIOR APPLICATION NUMBER: 09/166,170
 PRIOR FILING DATE: 1998-11-04

NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 18
 LENGTH: 33
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
 OTHER INFORMATION: Sequence submitted with "14" and "15"
 OTHER INFORMATION: Proteins through the cell membrane into the cell
 PUBLICATION INFORMATION:
 AUTHORS: Rojas, M. et al.
 TITLE: "Genetic Engineering of Proteins with Cell Membrane
 TITLE: Permeability"
 JOURNAL: Nature Biotechnology
 VOLUME: 16
 ISSUE: April
 PAGES: 370-375
 DATE: 1998-04-01
 US-09-562-868-18

Query Match 46.78 Score 14, DB 4, Length 33
 Best Local Similarity: 100.00, Pct ID: 100.00
 Matches: 14, Conservative: 0, Mismatches: 0, Indels: 0, Gaps: 0

QY 6 TCGGCGACAGAGAA 19
 DB 30 TCGGCGACAGAGAA 17

RESULT 12

US-09-870-930-56
 Sequence ID: 56, Alignment: 100.00, Score: 46.78
 Patent No. 6432680
 GENERAL INFORMATION:
 APPLICANT: HERSCA CARLOS, LARRY GARY, PAUL J. JOHNSON, CHARLIS VANDERHART, MI MIAMI
 TITLE OF INVENTION: "VASCULAR ENDOTHELIAL GROWTH FACTOR VEGF
 TITLE OF INVENTION: "VEGF AND ITS RECEPTORS
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Swanson and Bratschun, L.L.C.
 STREET: 9400 East Prentice Avenue, Suite #200
 CITY: Denver
 STATE: Colorado
 COUNTRY: USA
 ZIP: 80111
 CONTACT FEATURES: ECM,
 MEDIUM TYPE: Diskette, 3.5 inch, 1.4 MB storage
 COMPUTER: IBM compatible
 OPERATING SYSTEM: MS DOS
 SOFTWARE: WordPerfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-09-870,930
 FILING DATE: 6 JUNE 1997
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Barry J. Swanson
 REGISTRATION NUMBER: 33,215
 REFERENCE/INVENT NUMBER: NEX01
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 793-3333
 TELEFAX: (303) 793-9433
 INFORMATION FOR SEQ ID NO: 56:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 28
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: RNA
 FEATURE:
 OTHER INFORMATION: All primers are 2' fluoro

Best Local Similarity 100.0%, Seed No. 116-03,
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCGGCGACAGAGAA 19
|||||

DB 27 TCGGCGACAGAGAA 14

RESULT 7
US-09-186-170-14
Sequence 14, Application US/09/186170
Patent No. 6248558
GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6432680
TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: 22600.009702
CURRENT APPLICATION NUMBER: US/09/186170
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 60/080,083
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 09/186,170
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 17
LENGTH: 30
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: sequence encoding peptide which transports
OTHER INFORMATION: proteins through the cell membrane into the cell
EXPLANATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-186-170-14

Query Match 46.7%, Score 14, DB 4, Length 33;
Best Local Similarity 100.0%, Seed No. 116-03,
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCGGCGACAGAGAA 19
|||||

DB 27 TCGGCGACAGAGAA 14

RESULT 8
US-09-186-170-14
Sequence 14, Application US/09/186170
Patent No. 6248558
GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248558
TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: US/09/186170
CURRENT APPLICATION NUMBER: US/09/186,170
CURRENT FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/080,083
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 09/186,170
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 18
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: sequence encoding peptide which transports
OTHER INFORMATION: proteins through the cell membrane into the cell
EXPLANATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-186-170-14

Patent Filing Date: 1998-03-31
Number of Seq ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: sequence encoding peptide which transports
OTHER INFORMATION: proteins through the cell membrane into the cell
EXPLANATION INFORMATION:
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-186-170-14

Query Match 46.7%, Score 14, DB 4, Length 33;
Best Local Similarity 100.0%, Seed No. 116-03,
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 TCGGCGACAGAGAA 19
|||||

DB 33 TCGGCGACAGAGAA 20

RESULT 9
US-09-186-170-18/C
Sequence 18, Application US/09/186170
Patent No. 6248558
GENERAL INFORMATION:
APPLICANT: Lin, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248558
TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: US/09/186170
CURRENT APPLICATION NUMBER: US/09/186,170
CURRENT FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: 60/080,083
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 09/186,170
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 18
LENGTH: 33
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nucleotide
OTHER INFORMATION: sequence encoding peptide which transports
OTHER INFORMATION: proteins through the cell membrane into the cell
EXPLANATION INFORMATION:
AUTHORS: Rojas, M. et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
TITLE: Permeability"
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
US-09-186-170-18

Query Match 46.7%, Score 14, DB 4, Length 33;
Best Local Similarity 100.0%, Seed No. 116-03,
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

US-09-562-969-19

Query Match: 46.73, Score 11, DB 4, Length 24,
Best Local Similarity: 100.0%, Filed No. 1998-03-31
Matches: 14, Conserved: 0, Mismatched: 0, 16bits 0, gaps 0

CY 6 TGGCGCAGAGAGAA 19

DB 21 TGGCGCAGAGAGAA 8

RESULT 4

US-09-562-969-19

Sequence 16, Applicant: "Genetic Engineering"
Patent No. 6248558

GENERAL INFORMATION:

APPLICANT: Lin, Yao-Zhong

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

Patent No. 6248558

TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"

CURRENT APPLICATION NUMBER: US/09/186,170

CURRENT FILING DATE: 1998-11-04

EARLIER APPLICATION NUMBER: 09/090,083

EARLIER FILING DATE: 1998-02-31

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding protein which transports

OTHER INFORMATION: Proteins through the cell membrane into the cell

PUBLICATION INFORMATION:

TITLE: "Genetic Engineering of Proteins with Cell Membrane

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-375

DATE: 1998-04-01

RELEVANT RESIDUES: 1 TO 12

US-09-186-170-16

Query Match: 46.73, Score 11, DB 1, Length 27,
Best Local Similarity: 100.0%, Filed No. 1998-03-31
Matches: 14, Conserved: 0, Mismatched: 0, 16bits 0, gaps 0

CY 6 TGGCGCAGAGAGAA 19

DB 24 TGGCGCAGAGAGAA 11

RESULT 5

US-09-562-969-19

Sequence 16, Applicant: "Genetic Engineering"
Patent No. 6248558

GENERAL INFORMATION:

APPLICANT: Lin, Yao-Zhong

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

APPLICANT: Tan, Zhongjia

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

Patent No. 6248558

TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"

CURRENT APPLICATION NUMBER: US/09/186,170

CURRENT FILING DATE: 1998-11-04

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 16

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding protein which transports

OTHER INFORMATION: Proteins through the cell membrane into the cell

PUBLICATION INFORMATION:

TITLE: "Genetic Engineering of Proteins with Cell Membrane

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-375

DATE: 1998-04-01

RELEVANT RESIDUES: 1 TO 12

US-09-186-170-17

PRIOR APPLICATION NUMBER: 09/090,083
PRIOR FILING DATE: 1998-03-31
PUB. APPLICATION NUMBER: 09/090,170
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 16

LENGTH: 27

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding protein which transports

OTHER INFORMATION: Proteins through the cell membrane into the cell

PUBLICATION INFORMATION:

TITLE: "Genetic Engineering of Proteins with Cell Membrane

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-375

DATE: 1998-04-01

US-09-562-969-16

Query Match: 46.73, Score 11, DB 4, Length 27,
Best Local Similarity: 100.0%, Filed No. 1998-03-31
Matches: 14, Conserved: 0, Mismatched: 0, 16bits 0, gaps 0

CY 6 TGGCGCAGAGAGAA 19

DB 24 TGGCGCAGAGAGAA 11

RESULT 6

US-09-186-170-17

Sequence 16, Applicant: "Genetic Engineering"
Patent No. 6248558

GENERAL INFORMATION:

APPLICANT: Lin, Yao-Zhong

APPLICANT: Donahue, John P.

APPLICANT: Rojas, Mauricio

TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of

Patent No. 6248558

TITLE OF INVENTION: "Proteins with Cell Membrane Translocating Activity"

CURRENT APPLICATION NUMBER: US/09/186,170

CURRENT FILING DATE: 1998-11-04

EARLIER APPLICATION NUMBER: 09/090,083

EARLIER FILING DATE: 1998-02-31

NUMBER OF SEQ ID NOS: 18

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 17

LENGTH: 30

TYPE: DNA

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Nucleotide

OTHER INFORMATION: Sequence encoding protein which transports

OTHER INFORMATION: Proteins through the cell membrane into the cell

PUBLICATION INFORMATION:

TITLE: "Genetic Engineering of Proteins with Cell Membrane

JOURNAL: Nature Biotechnology

VOLUME: 16

ISSUE: April

PAGES: 370-375

DATE: 1998-04-01

RELEVANT RESIDUES: 1 TO 12

US-09-186-170-17

Query Match: 46.73, Score 11, DB 4, Length 27,

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977 10.2 34.0 30 4 US-09-031-192-19 Sequence 39, Appl
C 978 10.2 34.0 30 4 US-09-216-288-24 Sequence 34, Appl
C 979 10.2 34.0 30 4 US-09-401-474-54 Sequence 54, Appl
980 10.2 34.0 30 4 US-09-678-490-24 Sequence 32, Appl
C 981 10.2 34.0 31 1 US-07-921-7178-1 Sequence 1, Appl
C 982 10.2 34.0 31 1 US-07-779-444-1 Sequence 1, Appl
C 983 10.2 34.0 31 1 US-08-119-2628-1 Sequence 1, Appl
C 984 10.2 34.0 31 1 US-08-446-486-27 Sequence 27, Appl
C 985 10.2 34.0 31 1 US-08-135-9294-1 Sequence 1, Appl
C 986 10.2 34.0 31 1 US-08-234-265A-1 Sequence 1, Appl
C 987 10.2 34.0 31 1 US-08-463-308-27 Sequence 27, Appl
C 988 10.2 34.0 31 1 US-08-463-308-27 Sequence 27, Appl
C 989 10.2 34.0 31 1 US-09-142-952-92 Sequence 89, Appl
C 990 10.2 34.0 31 1 US-09-129-129-89 Sequence 89, Appl
C 991 10.2 34.0 31 2 US-08-739-167-84 Sequence 84, Appl
C 992 10.2 34.0 31 3 US-09-404-796-84 Sequence 84, Appl
C 993 10.2 34.0 31 3 US-08-931-869-86 Sequence 89, Appl
C 994 10.2 34.0 31 3 US-08-578-666C-5 Sequence 5, Appl
C 995 10.2 34.0 31 4 US-08-094-485-5 Sequence 5, Appl
996 10.2 34.0 31 3 US-08-410-832-54 Sequence 54, Appl
C 997 10.2 34.0 31 3 US-09-009-913-199 Sequence 199, Appl
C 998 10.2 34.0 31 3 US-09-144-112-5 Sequence 5, Appl
C 999 10.2 34.0 31 4 US-08-895-981-5 Sequence 5, Appl
C1000 10.2 34.0 31 4 US-09-450-444-54 Sequence 54, Appl

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ALIGNMENTS

RESULT 1

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US-09-257-544-11/c
Sequence 14, Application US/09257584A
Patent No. 6197611

```

```

GENERAL INFORMATION:
APPLICANT: Rice, Douglas A.
TITLE OF INVENTION: Constitutive Maize Promoters
FILE REFERENCE: 7719 31, 09/09/19701A
CURRENT APPLICATION NUMBER: 09/032571, 84A
CURRENT FILING DATE: 1999-02-25
EARLIER APPLICATION NUMBER: 09/0304, 07A
EARLIER FILING DATE: 1998-02-26
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 13
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Maize
US-09-257-544-11

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Query Match 47 %; Score 14.2; DB 4; Length 27;
Best Local Similarity 94.2%; Seed No. 8, 54, 102;
Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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```

UY 1 GTATTGCGACAGAGAA 19
DB 20 GAAAGTGGCGAAGAGTA 2

```

```

RESULT 2
US-09-186-170-15/c
Sequence 15, Application US/09186170
Patent No. 6248548
GENERAL INFORMATION:
APPLICANT: Tan, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6248548
TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"

```

```

FILE REFERENCE: US9841
CURRENT APPLICATION NUMBER: US/09186170
CURRENT FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 09/0304, 07A
EARLIER FILING DATE: 1998-02-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 15
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nuclear lip
OTHER INFORMATION: Sequence encoding peptides which transp
OTHER INFORMATION: Proteins through the cell membrane into the cell
PUBLICATION INFORMATION:
AUTHORS: Rojas, M et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01
RELEVANT RESOURCES: 1 TO 12
US-09-186-170-15

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Query Match 46.7%; Score 14; DB 4; Length 24;
Best Local Similarity 100.0%; Seed No. 1e+01;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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UY 5 TGGGCAAGAGAGAA 19
DB 21 TGGGCAAGAGAGAA 8

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RESULT 3
US-09-570-868-15/c
Sequence 15, Application US/09570868
Patent No. 6432680
GENERAL INFORMATION:
APPLICANT: Tan, Yao-Zhong
APPLICANT: Donahue, John P.
APPLICANT: Rojas, Mauricio
APPLICANT: Tan, Zhongjia
TITLE OF INVENTION: "Sequence and Method for Genetic Engineering of
Patent No. 6432680
TITLE OF INVENTION: Proteins with Cell Membrane Translocating Activity"
FILE REFERENCE: 22099 090702
CURRENT APPLICATION NUMBER: 09/032571, 84A
CURRENT FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: 09/0060, 983
PRIOR FILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 09/186, 170
PRIOR FILING DATE: 1998-11-04
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 15
LENGTH: 24
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Nuclear lip
OTHER INFORMATION: Sequence encoding peptides which transp
OTHER INFORMATION: Proteins through the cell membrane into the cell
PUBLICATION INFORMATION:
AUTHORS: Rojas, M et al.
TITLE: "Genetic Engineering of Proteins with Cell Membrane
JOURNAL: Nature Biotechnology
VOLUME: 16
ISSUE: April
PAGES: 370-375
DATE: 1998-04-01

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701	10.4	34.7	22	17	US-09-890-363-1	Sequence 34, Affl
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703	10.4	34.7	22	19	US-09-890-363-1	Sequence 36, Affl
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705	10.4	34.7	22	21	US-09-890-363-1	Sequence 38, Affl
706	10.4	34.7	22	22	US-09-890-363-1	Sequence 39, Affl
707	10.4	34.7	22	23	US-09-890-363-1	Sequence 40, Affl
708	10.4	34.7	22	24	US-09-890-363-1	Sequence 41, Affl
709	10.4	34.7	22	25	US-09-890-363-1	Sequence 42, Affl
710	10.4	34.7	22	26	US-09-890-363-1	Sequence 43, Affl
711	10.4	34.7	22	27	US-09-890-363-1	Sequence 44, Affl
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716	10.4	34.7	22	32	US-09-890-363-1	Sequence 49, Affl
717	10.4	34.7	22	33	US-09-890-363-1	Sequence 50, Affl
718	10.4	34.7	22	34	US-09-890-363-1	Sequence 51, Affl
719	10.4	34.7	22	35	US-09-890-363-1	Sequence 52, Affl
720	10.4	34.7	22	36	US-09-890-363-1	Sequence 53, Affl
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722	10.4	34.7	22	38	US-09-890-363-1	Sequence 55, Affl
723	10.4	34.7	22	39	US-09-890-363-1	Sequence 56, Affl
724	10.4	34.7	22	40	US-09-890-363-1	Sequence 57, Affl
725	10.4	34.7	22	41	US-09-890-363-1	Sequence 58, Affl
726	10.4	34.7	22	42	US-09-890-363-1	Sequence 59, Affl
727	10.4	34.7	22	43	US-09-890-363-1	Sequence 60, Affl
728	10.4	34.7	22	44	US-09-890-363-1	Sequence 61, Affl
729	10.4	34.7	22	45	US-09-890-363-1	Sequence 62, Affl
730	10.4	34.7	22	46	US-09-890-363-1	Sequence 63, Affl
731	10.4	34.7	22	47	US-09-890-363-1	Sequence 64, Affl
732	10.4	34.7	22	48	US-09-890-363-1	Sequence 65, Affl
733	10.4	34.7	22	49	US-09-890-363-1	Sequence 66, Affl
734	10.4	34.7	22	50	US-09-890-363-1	Sequence 67, Affl
735	10.4	34.7	22	51	US-09-890-363-1	Sequence 68, Affl
736	10.4	34.7	22	52	US-09-890-363-1	Sequence 69, Affl
737	10.4	34.7	22	53	US-09-890-363-1	Sequence 70, Affl
738	10.4	34.7	22	54	US-09-890-363-1	Sequence 71, Affl
739	10.4	34.7	22	55	US-09-890-363-1	Sequence 72, Affl
740	10.4	34.7	22	56	US-09-890-363-1	Sequence 73, Affl
741	10.4	34.7	22	57	US-09-890-363-1	Sequence 74, Affl
742	10.4	34.7	22	58	US-09-890-363-1	Sequence 75, Affl
743	10.4	34.7	22	59	US-09-890-363-1	Sequence 76, Affl
744	10.4	34.7	22	60	US-09-890-363-1	Sequence 77, Affl
745	10.4	34.7	22	61	US-09-890-363-1	Sequence 78, Affl
746	10.4	34.7	22	62	US-09-890-363-1	Sequence 79, Affl
747	10.4	34.7	22	63	US-09-890-363-1	Sequence 80, Affl
748	10.4	34.7	22	64	US-09-890-363-1	Sequence 81, Affl
749	10.4	34.7	22	65	US-09-890-363-1	Sequence 82, Affl
750	10.4	34.7	22	66	US-09-890-363-1	Sequence 83, Affl
751	10.4	34.7	22	67	US-09-890-363-1	Sequence 84, Affl
752	10.4	34.7	22	68	US-09-890-363-1	Sequence 85, Affl
753	10.4	34.7	22	69	US-09-890-363-1	Sequence 86, Affl
754	10.4	34.7	22	70	US-09-890-363-1	Sequence 87, Affl
755	10.4	34.7	22	71	US-09-890-363-1	Sequence 88, Affl
756	10.4	34.7	22	72	US-09-890-363-1	Sequence 89, Affl
757	10.4	34.7	22	73	US-09-890-363-1	Sequence 90, Affl

[illegible]

Geneva version - 1,
Copyright (c) 1993 2003 CompuGen Ltd

On metrics - include search, using an external

Run on: July 21, 2008, 17:41:02; Search time 23.994 seconds
(without alignments)
400.117 Million cell updates/second

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1-228-60-50

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100	1

Searched: 441362 sots, 15000000 ref:1000000

Total number of MHC-activating ligand parameters: 43604

Maximum	05	seq	length: 0
Maximum	03	seq	length: 35

	Minimum Match	Maximum Match
Pre-processing:	0.0067	0.0089
Post-processing:	0.0067	0.0089

Listing first 1000 summaries

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Pred. No. 12 The method of finding the predicted score greater than or equal to the score of the result being printed and is derived by analyzing the results of both tests.

SUMMARY

[illegible]



DT 30-SEP-1993 (first entry)
 XX Thrombin inhibitor primer (11).
 DE Thrombin inhibitor primer (11).
 XX
 XX
 KM Primer: PCR, thrombosis, arterial reocclusion; blood; thrombin;
 KM hirudin; ss.
 XX
 OS Synthetic.
 XX
 PN DE4209110.A.
 XX
 PD 27-MAY-1993
 XX
 PF 20-MAR-1992; 92DE-4209110.
 XX
 PR 26-NOV-1991; 91E 413698
 PR 20-MAR-1992; 92DE-4209110.
 XX
 PA (BAD1) BASE AG.
 FI Biadjan S, Friedrich T, Fiediger E, Strube K
 DR WPL/ 2001-289718/30.
 XX
 PT New proteins obtd. from Haemaphysa sylvestris, used as thrombin
 PT inhibitor for treatment and prevention of thrombosis and
 PT arterial re-occlusion
 XX
 PS Example 6: Page 6; 14pp; German.
 XX
 CC Example 6 describes the cloning of cDNA encoding the thrombin
 CC inhibiting protein. A cDNA library is produced from H. sylvestris
 CC DNA. Primers (i) - AAQ42426 and (ii) - AAQ42427 were based on peptide
 CC fragments corresp. to amino acids 4-11 and 12-19 respectively.
 CC The 3' primers were A-B-T18 (AAQ42428), A (derived from A-B-T18 -
 CC AAQ42427) and B (derived from A-B-T18 - AAQ42430). A first sequence
 CC was obtained (AAQ42433). A further PCR cycle was performed using
 CC primers (iii - AAQ42431) and (iv - AAQ42432). The sequence
 CC given in AAQ42434 was obtained.
 XX
 SQ Sequence 23 BP; 5 A; 0 G; 7 C; 4 T; 7 others;
 XX
 Query Match 44.7%, Score 13.4; DB 23; Length 23;
 Best Local Similarity 54.5%; Pred. No. 1.8e+04;
 Matches 12; Conservative 6; Mismatch 4; Indels 0; Gaps 0;
 XX
 CY 1-ATGATTCCTCTTACGAGCAATTCG 22
 1-||||| 1-||||| 1-||| 1-|||
 2-ATGATTCCTCTTACGAGCAATTCG 22
 XX
 DE Thrombin inhibitor primer (11).
 XX
 AC AAH03101 standard; DNA; 25 BP.
 XX
 AC AAH03101;
 XX
 DT 15-JUN-2001 (first entry)
 XX
 DE Micro-sequencing detection method related oligonucleotide seq. IT NC0125
 DE M17 oligonucleotide (first entry) containing cDNA sequencing, RNA type,
 KM bi-directional sequencing; infection; mutation detection; PCR primer; ss.
 OS Unidentified.
 XX
 PN US6214555 B1.
 XX
 PD 10-APR-2001.
 XX
 PF 13-MAY-1999; 98US-0640672.
 XX
 PR 01-MAY-1996; 96US-0640672.

PR 19-JUL-1996; 96US-0684498.
 PR 22-FEB-1997; 97US-0807138.
 PR 20-JAN-1994; 94US-0009483.
 XX
 PA (VIST-) VISIBLE GENETICS INC.
 XX
 PI Leushner J, Hui M, Dunn JM, Lacroix J;
 DR WPL/ 2001-289718/30.
 XX
 PT Composition for detecting microorganisms, comprising deoxynucleotide
 PT triphosphate, deoxy-2',3'-bisphosphate, and thymidine
 PT polymerase to incorporate deoxynucleotide triphosphate into extended
 PT polymer.
 XX
 PS Disclosed: column 85; 62pp; English.
 XX
 CC The present invention provides a composition containing 4 dNTPs and at
 CC least one dNTP and a thermally stable polymerase which incorporation
 CC dNTPs into an extending nucleic acid polymer at a rate of not less than
 CC 0.4 times the rate of NTP incorporation. This can be used with the 1p
 CC primers provided in the invention to detect the presence of
 CC microorganisms, such as Chlamydia trachomatis, HIV or human
 CC papillomavirus, in a sample. In addition, it can be used to detect
 CC mutations in a specific gene, to determine RNA type, and to produce
 CC sequencing fragments for further study.
 XX
 SQ Sequence 25 BP; 8 A; 7 C; 3 G; 7 T; 0 others;
 XX
 Query Match 44.7%, Score 13.4; DB 22; Length 25;
 Best Local Similarity 53.3%; Pred. No. 1.8e+04;
 Matches 14; Conservative 1; Mismatch 1; Indels 0; Gaps 0;
 XX
 CY 13-ATGATTCCTCTTACGAGCAATTCG 22
 1-||||| 1-||||| 1-||| 1-|||
 24-ATGATTCCTCTTACGAGCAATTCG 22
 XX
 DE Thrombin inhibitor primer (11).
 XX
 AC AAF87823;
 XX
 DT 11-JUN-2001 (first entry)
 XX
 DE Human haemopoietic receptor protein NP12 PCR primer NP12 ST.
 XX
 KM Human haemopoietic receptor protein NP12, haemopoietic;
 KM anti-allergic; haemopoietic factor; autoimmune disease; tissue rejection;
 KM metal allergy; pollen allergy; PCR primer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200121556-A1.
 XX
 PD 05-APR-2001.
 XX
 PF 27-SEP-2000; 2000WO-0106654.
 XX
 PR 27-SEP-1999; 99JP-0271358.
 PR 13-AUG-2000; 00US-0240397.
 XX
 PA (CHUGAI) CHUGAI RES. INST. MOLECULAR MEDICINE INC.
 XX
 PI Maeda M, Yaguchi N;
 DR WPL/ 2001-266154/27.
 XX
 PT New hemopoietin receptor protein NP12 useful for screening for new
 PT binding factors for potential treatment of autoimmune disease, tissue
 PT rejection and allergies.

ID AA228757 standard, DNA; 33 BP.
 AC AA228757.
 XX
 XX
 DT 01-FEB-2000 (first entry)
 DE Truncated membrane-translocating peptide sequence coding region #8.
 XX
 XX Membrane-translocating peptide sequence; MTS; fusion protein; production;
 XX Schistosoma japonicum; glutathione S transferase; adenovirus; mammal;
 XX p53; immune response; hepatitis B virus; surface antigen; canine; feline;
 XX protease inhibitor; cancer; tumor suppressor; bovine; ss
 XX
 OS Synthetic.
 XX
 XX W09949879-A1.
 XX
 XX 07-OCT-1999.
 XX
 XX 31-MAR-1999; 99WO-0507189.
 XX
 XX 31-MAR-1999; 98US-0000083.
 XX 04-NOV-1998; 98US-0186170.
 XX
 XX (UYVA-) UNIV VANDERBILT.
 XX
 XX Lin Y, Donahue JP, Rojas M, Tan ZJ.
 XX
 XX WPI: 1999.610819/52.
 XX P-PSUR: AAV44160.
 XX
 XX New peptides containing a membrane-translocating sequence used to
 XX develop products for use in, e.g. vaccines.
 XX
 XX Disclosure, Page 9, 85pp; English.
 XX
 XX Sequence AA228757 represents truncated coding regions based on
 XX the coding region of a novel membrane-translocating peptide sequence
 XX (MTS, AA228749). The invention relates to the use of the MTS peptides
 XX for generating fusion proteins which can be used for the production of
 XX polypeptides of interest such as a viral polypeptide such as
 XX transferrin, an adenovirus E3 19k protein or a mammalian p53 protein.
 XX Fusions of the peptides can also be used for inducing an immune response
 XX in a mammal using such a viral polypeptide such as hepatitis B
 XX surface antigen. They can also be used for protecting a subject from an
 XX infectious agent using a polypeptide that inhibits reproduction of the
 XX infectious agent such as a protease inhibitor. They can also be used for
 XX treating a subject using a polypeptide that suppresses such as p53 protein
 XX or a polypeptide inhibitor of Bcl-2. The methods can be used for
 XX treating canine, feline and bovine diseases and also for studying
 XX intracellular proteins.
 XX
 XX Sequence 33 BP; 1 A, 15 C, 5 G, 12 T, 0 other;
 XX
 XX Query Match 46.7%, Score 14, DB 20, Length 33,
 XX Best Local Similarity 100.0%, Pred. No. 1e-04;
 XX Matches 14; Conservation 0, Mismatches 0, Indels 0, Gaps 0,
 XX
 XX QY 6 TGGGCAAGAGAA 19
 XX |||||||||
 XX 10 TGGGCAAGAGAA 17
 XX
 XX RESULT 24
 XX AA228749/
 XX ID AA228749 standard, DNA; 34 BP.
 XX
 XX AC AA228749;
 XX
 XX DT 01-FEB-2000 (first entry)
 XX
 XX DE Membrane-translocating peptide sequence coding region.
 XX
 XX XX

XX Membrane-translocating peptide sequence; MTS; fusion protein; production;
 XX Schistosoma japonicum; glutathione S transferase; adenovirus; mammal;
 XX p53; immune response; hepatitis B virus; surface antigen; canine; feline;
 XX protease inhibitor; cancer; tumor suppressor; bovine; ss
 XX
 OS Synthetic.
 XX
 XX W09949879-A1.
 XX
 XX 07-OCT-1999.
 XX
 XX 31-MAR-1999; 99WO-0507189.
 XX
 XX 31-MAR-1999; 98US-0000083.
 XX 04-NOV-1998; 98US-0186170.
 XX
 XX (UYVA-) UNIV VANDERBILT.
 XX
 XX Lin Y, Donahue JP, Rojas M, Tan ZJ.
 XX
 XX WPI: 1999.610819/52.
 XX P-PSUR: AAV44160.
 XX
 XX New peptides containing a membrane-translocating sequence used to
 XX develop products for use in, e.g. vaccines.
 XX
 XX Disclosure, Page 8, 85pp; English.
 XX
 XX This sequence represents the coding region for a novel membrane-
 XX translocating peptide sequence (MTS). The invention relates to the use
 XX of the MTS peptides for generating fusion proteins which can be used for
 XX the production of polypeptides of interest such as a viral polypeptide
 XX such as transferrin, an adenovirus E3 19k protein or a mammalian
 XX p53 protein. Fusions of the peptides can also be used for inducing an
 XX immune response in a mammal using e.g. a viral polypeptide such as
 XX hepatitis B surface antigen. They can also be used for protecting a
 XX subject from an infectious agent using a polypeptide that inhibits
 XX reproduction of the infectious agent such as a protease inhibitor.
 XX They can also be used for treating cancer using a polypeptide that
 XX suppresses such as p53 protein or a polypeptide inhibitor of Bcl-2.
 XX The methods can be used for studying intracellular proteins.
 XX
 XX Sequence 34 BP; 2 A, 14 C, 6 G, 12 T, 0 other;
 XX
 XX Query Match 46.7%, Score 14, DB 20, Length 34,
 XX Best Local Similarity 100.0%, Pred. No. 1e-04;
 XX Matches 14; Conservation 0, Mismatches 0, Indels 0, Gaps 0,
 XX
 XX QY 6 TGGGCAAGAGAA 19
 XX |||||||||
 XX 33 TGGGCAAGAGAA 20
 XX
 XX RESULT 25
 XX AA24187/
 XX ID AA24187 standard, DNA; 20 BP.
 XX
 XX AC AA24187;
 XX
 XX DT 13-SEP-1999 (first entry)
 XX
 XX DE PCR primer used to amplify an ORF of Chlamydia pneumoniae.
 XX
 XX XX Respiratory disease; pneumonia; bronchitis; heart disease; streptococcus;
 XX sinusitis; paratubercular infection; cytomegalovirus; pharyngitis;
 XX vaccine; neutralizing epitope; PCR primer; ss.
 XX
 OS Synthetic.
 OS Chlamydia pneumoniae.
 XX
 XX W09927105-A2.
 XX

CC treating canine, feline and bovine diseases and also for studying
 CC intracellular proteins.

SC Sequence 26 BP, 1 A, 12 C, 3 G, 10 T, 0 other;

Query Match 46.7% Score 14; DB 20; Length 26;
 Best Local Similarity 100.0%; Pred No. 1e+04;
 Matches 14; Conservative 0; Mismatched 0; Table 0; Page 0;

CY 6 TGGCGCAGAGAGAA 19
 |||||
 DB 24 TGGCGCAGAGAGAA 11

RESULT 21
 AA228756/c
 ID AA228756 standard, cna, 30 BP.

AC AA228756;

DT 01-FEB-2000 (first entry)

DE Truncated membrane-translocating peptide sequence coding region #7.

XX Membrane translocating peptide sequence; MTS; fusion protein; production;
 XX Schistosoma japonicum; giardiasis; transferrin; adenovirus; human;
 XX P53; immune response; hepatitis B virus; surface antigen; canine; feline;
 XX protease inhibitor; cancer; tumor suppressor; bovine; cat.

XX Synthetic.

XX W09949879-A1.

XX 07-OCT-1999.

XX 31-MAR-1999; 9800-US07189.

XX 31-MAR-1999; 9800-US07189.

XX 04-NOV-1999; 9800-US07189.

XX (UYVA) UNIV VANDERBILT

XX Lin Y, Donahue JP, Rojas M, Tan ZJ;

XX WPI; 1999-610819/52.

XX F-PDB; AAY44167.

XX New peptides containing a membrane-translocating sequence used for
 XX detecting products for use in, e.g., vaccines.

XX Disclosures; Page 9; 85pp; English.

XX Sequences AA228756 and 20 represent truncated coding regions based on
 CC the coding region of a novel membrane-translocating peptide sequence
 CC (MTS; AA228756). The invention relates to the use of the MTS peptide
 CC for generating fusion proteins which can be used for the production of
 CC polypeptides of interest such as a protein or a mammalian P3 protein.
 CC Transferrin, an adenovirus P3 protein or a mammalian P3 protein
 CC fusions of the peptides can also be used for inducing an immune response
 CC in a mammal using e.g. a viral polypeptide such as hepatitis B
 CC surface antigen. They can also be used for inducing a strong B
 CC infection agent using a polypeptide that inhibits reproduction of the
 CC infectious agent such as a polypeptide inhibitor. They can also be used for
 CC treating cancer using a polypeptide tumor suppressor such as P53 protein
 CC or a polypeptide inhibitor of P53 protein. The methods can be used for
 CC treating canine, feline and bovine diseases and also for studying
 CC intracellular proteins.

SC Sequence 30 BP, 1 A, 13 C, 4 G, 12 T, 0 other;

Query Match 46.7% Score 14; DB 20; Length 30;
 Best Local Similarity 100.0%; Pred No. 1e+04;
 Matches 14; Conservative 0; Mismatched 0; Table 0; Page 0;

CY 6 TGGCGCAGAGAGAA 19
 |||||
 DB 27 TGGCGCAGAGAGAA 14

RESULT 22
 AA228753/c
 ID AA228753 standard, cna, 32 BP.

AC AA228753;

DT 01-FEB-2000 (first entry)

DE Truncated membrane-translocating peptide sequence coding region #4.

XX Membrane translocating peptide sequence; MTS; fusion protein; production;
 XX Schistosoma japonicum; giardiasis; transferrin; adenovirus; human;
 XX P53; immune response; hepatitis B virus; surface antigen; canine; feline;
 XX protease inhibitor; cancer; tumor suppressor; bovine; cat.

XX Synthetic.

XX W09949879-A1.

XX 07-OCT-1999.

XX 31-MAR-1999; 9800-US07189.

XX 31-MAR-1999; 9800-US07189.

XX 04-NOV-1999; 9800-US07189.

XX (UYVA) UNIV VANDERBILT

XX Lin Y, Donahue JP, Rojas M, Tan ZJ;

XX WPI; 1999-610819/52.

XX F-PDB; AAY44164.

XX New peptides containing a membrane-translocating sequence used for
 XX detecting products for use in, e.g., vaccines.

XX Disclosures; Page 9; 85pp; English.

XX Sequences AA228753 and 20 represent truncated coding regions based on
 CC the coding region of a novel membrane-translocating peptide sequence
 CC (MTS; AA228753). The invention relates to the use of the MTS peptide
 CC for generating fusion proteins which can be used for the production of
 CC polypeptides of interest such as a protein or a mammalian P3 protein.
 CC Transferrin, an adenovirus P3 protein or a mammalian P3 protein
 CC fusions of the peptides can also be used for inducing an immune response
 CC in a mammal using e.g. a viral polypeptide such as hepatitis B
 CC surface antigen. They can also be used for inducing a strong B
 CC infection agent using a polypeptide that inhibits reproduction of the
 CC infectious agent such as a polypeptide inhibitor. They can also be used for
 CC treating cancer using a polypeptide tumor suppressor such as P53 protein
 CC or a polypeptide inhibitor of P53 protein. The methods can be used for
 CC treating canine, feline and bovine diseases and also for studying
 CC intracellular proteins.

SC Sequence 32 BP, 1 A, 13 C, 4 G, 12 T, 0 other;

Query Match 46.7% Score 14; DB 20; Length 32;
 Best Local Similarity 100.0%; Pred No. 1e+04;
 Matches 14; Conservative 0; Mismatched 0; Table 0; Page 0;

CY 6 TGGCGCAGAGAGAA 19
 |||||
 DB 33 TGGCGCAGAGAGAA 20

RESULT 23
 AA228757/c

PI Lin Y, Donahue JP, Rojas M, Tan ZJ;
 XX
 TF WFI, 1999-610919/52
 DR P-PSDB; AAY44165.
 XX
 PT New peptides containing a membrane translocating sequence used to
 FT develop products for use in, e.g., vaccines.
 XX
 PS Disclosure, Page 9; 85pp; English.
 XX
 CC Sequences AAZ28755-229977 represent truncated coding regions based on
 CC the coding region of a novel membrane-translocating peptide sequence
 CC (MTR; AAZ28755). The invention relates to the use of the MTR peptides
 CC for generating fusion proteins which can be used for the production of
 CC polypeptides of interest such as Schistosoma japonicum glutathione S
 CC transferase, an adenovirus E1 19k protein or a mammalian p53 protein.
 CC Fusions of the peptides can also be used for inducing an immune response
 CC in a mammal using e.g., a viral polypeptide such as hepatitis B
 CC surface antigen. They can also be used for protecting a subject from an
 CC infectious agent using a polypeptide that inhibits reproduction of the
 CC infectious agent such as a protease inhibitor. They can also be used for
 CC treating cancer using a polypeptide tumor suppressor such as p53 protein
 CC or a Bcl-2 inhibitor. The peptides can be used for
 CC treating cancer, killing and lysing tumorous and non-tumorous
 CC intracellular proteins.
 XX
 SO Sequence 24 BP; 1 A; 12 C; 4 G; 8 T; 0 Other;
 XX
 Query Match: 46 78; Score 14; DR 24; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9,88+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 CY 6 TGGCGGACAGAGAA 19
 DB 21 TGGCGGACAGAGAA 8
 XX
 RESULT 19
 ARL61515
 ID ARL61515 standard; DNA; 24 BP.
 XX
 AC ARL61515;
 XX
 DT 13-SEP-2002 (first entry)
 XX
 DE Human endoplasmic reticulum 11-66 H175 protein (p21)
 XX
 KW Endoplasmic reticulum 11-66 malignant tumour; haemophagocytic HIV infection;
 KW human immune deficiency virus; immunological disorder; inflammation;
 KW human; PCR; primers; ss.
 XX
 OS Homo sapiens.
 XX
 PR CNI313746 A.
 XX
 PD 27 MAR 2002.
 XX
 PF 07 SEP-2000; 2000CN-0125087.
 XX
 PR 07 SEP-2000; 2000CN-0125087.
 XX
 PA (SWAN) : SWAN:MAI RI:GCGG GERE GVE GQ LIG.
 XX
 PI Mao Y, Xin Y.
 XX
 DR WPI; 2002-509473/55
 XX
 PT New polypeptide human endoplasmic reticulum 11-66 protein containing malignant
 PT tumor, hemophagocytic human immunodeficiency virus infection, immunology and
 PT disease and various inflammations
 XX
 PD Example 1, Page 17, 13pp; Chinese.

CC This invention describes a novel human endoplasmic reticulum 11-66, the
 CC polypeptide encoding the polypeptide and a method of producing the
 CC polypeptide by using DNA recombinant technology. The invention also
 CC discloses curing several diseases, such as malignant tumors, hemophagocytic
 CC human immunodeficiency virus (HIV) infection, immunological disease and
 CC various inflammations using the polypeptide. The invention also discloses
 CC an antagonist for treating the polypeptide and its treatment in animals.
 CC This sequence represents a RT-PCR primer used in the amplification of the
 CC human endoplasmic reticulum 11-66 gene described in the disclosure of the
 CC invention.
 XX
 SO Sequence 24 BP; 5 A; 3 C; 4 G; 8 T; 1 Other;
 XX
 Query Match: 46 78; Score 14; DR 24; Length 24;
 Best Local Similarity 100.0%; Pred. No. 9,88+03;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 CY 4 ATTGGGTAATGAAATTTT 25
 DB 3 ATTGGGTAATGAAATTTT 24
 XX
 RESULT 23
 AAC28755/C
 ID AAC28755 standard; DNA; 26 BP.
 XX
 AC AAC28755;
 XX
 DT 01 FEB 2002 (first entry)
 XX
 DE Truncated membrane-translocating peptide sequence coding region #5.
 XX
 KW Membrane-translocating peptide sequence; MTR; fusion protein; production;
 KW Schistosoma japonicum; glutathione S transferase; adenovirus; mammalian
 KW p53; immune response; hepatitis B virus; surface antigen; cancer; tumor;
 KW protease inhibitor; cancer; liver; efficiency; protein; ss.
 XX
 OS Synthetic.
 XX
 PR WO9949879-A1.
 XX
 PD 07-OCT-1999.
 XX
 PF 41-MAR-1999; WWW-01807189.
 XX
 DE 41-MAR-1999; WWW-01807189.
 XX
 PR 04-NOV-1998; WWW-01807189.
 XX
 PA (TIVA) : UNIV VANDERBILT.
 XX
 PI Lin Y, Donahue JP, Rojas M, Tan ZJ;
 XX
 DR WPI; 1999-610919/52.
 XX
 PF P-PSDB; AAY44165.
 XX
 PT New peptides containing a membrane translocating sequence used to
 FT develop products for use in, e.g., vaccines.
 XX
 PS Disclosure, Page 9; 85pp; English.
 XX
 CC Sequences AAZ28755-229977 represent truncated coding regions based on
 CC the coding region of a novel membrane translocating peptide sequence
 CC (MTR; AAZ28755). The invention relates to the use of the MTR peptides
 CC for generating fusion proteins which can be used for the production of
 CC polypeptides of interest such as Schistosoma japonicum glutathione S
 CC transferase, an adenovirus E1 19k protein or a mammalian p53 protein.
 CC Fusions of the peptides can also be used for inducing an immune response
 CC in a mammal using e.g., a viral polypeptide such as hepatitis B
 CC surface antigen. They can also be used for protecting a subject from an
 CC infectious agent using a polypeptide that inhibits reproduction of the
 CC infectious agent such as a protease inhibitor. They can also be used for
 CC treating cancer using a polypeptide tumor suppressor such as p53 protein
 CC or a Bcl-2. The methods can be used for

CC phenotypic. The reference RNA transcript would bind to native mRNA and
 CC interfere with translation.

XX Sequence 27 BP; 4 A; 8 C; 6 G; 9 T; 0 other;

Query Match 47.3% Score 14.2; DE 20; Length 27;
 Best Local Similarity 84.2%; Pred. No. 8,10+03;
 Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATATTTCTTCTTATATATGA 19
 DB 20 CCAATTCGCGACAGAGATA 2

RESULT 14
 ABL99409/C
 ID ABL99409 standard, DNA, 27 BP.

XX ABL99409;

AC 02-JUL-2002 (first entry)

XX Right PCR primer used to target ubiquitin canine gene.

XX Canine gene array, toxicological responses; ss.

XX Canis sp.

XX WO200208453-A2.

XX 31 JAN 2002.

XX 23-JUL-2001; 2001WO US23511.

XX 21-JUL-2000; 2000US-220057P.

XX (PHASE-1) MOLECULAR TOXICOLOGY.

XX Fast SP, Picked; 93, Neft PE, Dunn RT;

XX WPI; 2002 action/27;

XX Identifying toxicologically relevant canine gene to determine

XX toxicology in response of apoptosis by standard and comparing gene

XX expression profiles of untreated canine cells and canine cells treated

XX with an agent.

XX Example 1, Page 10, 140BP, English.

XX This invention relates to identifying a toxicologically relevant canine

XX gene and the generation of an array of toxicologically relevant

XX canine genes. The gene array is useful for obtaining a gene expression

XX profile, by operating a population of cells with an agent, obtaining cDNA

XX from the population of cells, labeling the cDNA, and contacting the cDNA

XX arrays to determine toxicological responses to various agents, and also

XX CC The method for analyzing toxicological responses using the canine

XX gene array is rapid and efficient. The present sequence is related

XX to the canine gene array.

XX

AAE0805
 ID AAE0805 standard, DNA, 30 BP.

XX AAE0805;

XX 21 JUN 2001 (first entry)

XX Hydanoloin racemase gene PCR primer S1138.

XX Hydanoloin racemase, hyda gene, amino carboxylic acid PCR primer;

XX ss.

XX Archaeobacter aureusens.

XX WO200123525 A2.

XX 05 APR 2001.

XX 02-SEP-2000; 2000WO-EP08580.

XX 27-SEP-1999; 99EP-0118956.

XX (DECS) DEQUSSA-HUBIS AG.

XX (UYST-) UNIV STUTTGART.

XX (HGEF) RECHT TACHENSTES GMBH.

XX Alenbuchner J, Maties R, Pietzsch M, Sydatk C, Wiese A;

XX Bommaritus A, Tischer W;

XX WPI; 2001-281641/29.

XX Novel rec-Hydanoloin-racemase from Archaeobacter aureusens DSM 1737

XX (hyda) useful for producing enantiomerically enriched amino carboxylic

XX acids or its derivatives on industrial scale.

XX Example; Page 8; 21pp; English.

XX The present sequence is that of primer S1138, designed for the

XX PCR amplification of the hydanoloin racemase gene (hyda, see

XX AAE0805) of Archaeobacter aureusens DSM 1737. S1138 was used with

XX primer S1137 (see AAE0805) for the PCR, with pMT6 as template.

XX The PCR product was inserted into expression vector pRBE2702,

XX creating E. coli strain pRBE2702, which was utilized in the production of

XX recombinant hydanoloin racemase in Escherichia coli JM109

XX transformants. A primer for the gene encoding the hydanoloin

XX racemase is claimed. The recombinant enzyme is able to racemize

XX hydanoloin under physiological conditions with a rate acceptable

XX for implementation in an industrial scale. It was use of the

XX racemase in processes for the production of amino carboxylic acids

XX or their derivatives, and of enantiomerically enriched compounds.

XX conducted in an enzyme mediated process is also claimed.

XX Sequence to Ref. A A, 7 C, 10 G, 8 T, 6 other;

XX Sequence to Ref. A A, 7 C, 10 G, 8 T, 6 other;

Query Match 47.3% Score 14.2; DE 20; Length 30;

Best Local Similarity 70.4%; Pred. No. 8,20+03;

Matches 19; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 3 AATTCGCGACAGAGATA 29

DB 3 AACTGCGCGACAGAGATA 29

AA208548/C

AA208548; 02-SEP-1999 (first entry)

XX Parathyroid hormone receptor reverse transcriptase PCR primer #1.

XX

XX

AA078196/196/c 48 bp Score 14.61 DB 23 Length 35
 Query Match: 48 bp Score 14.61 DB 23 Length 35
 Seed Match: 48 bp Score 14.61 DB 23 Length 35
 Match: 48 bp Score 14.61 DB 23 Length 35
 Sequence 35 BP: 8 A 6 G 9 G 12 T 0 other

AA078196/196/c 48 bp Score 14.61 DB 23 Length 35
 Query Match: 48 bp Score 14.61 DB 23 Length 35
 Seed Match: 48 bp Score 14.61 DB 23 Length 35
 Match: 48 bp Score 14.61 DB 23 Length 35
 Sequence 35 BP: 8 A 6 G 9 G 12 T 0 other

AA078196/196/c 48 bp Score 14.61 DB 23 Length 35
 Query Match: 48 bp Score 14.61 DB 23 Length 35
 Seed Match: 48 bp Score 14.61 DB 23 Length 35
 Match: 48 bp Score 14.61 DB 23 Length 35
 Sequence 35 BP: 8 A 6 G 9 G 12 T 0 other

AA078196/196/c 48 bp Score 14.61 DB 23 Length 35
 Query Match: 48 bp Score 14.61 DB 23 Length 35
 Seed Match: 48 bp Score 14.61 DB 23 Length 35
 Match: 48 bp Score 14.61 DB 23 Length 35
 Sequence 35 BP: 8 A 6 G 9 G 12 T 0 other

AA078196/196/c 48 bp Score 14.61 DB 23 Length 35
 Query Match: 48 bp Score 14.61 DB 23 Length 35
 Seed Match: 48 bp Score 14.61 DB 23 Length 35
 Match: 48 bp Score 14.61 DB 23 Length 35
 Sequence 35 BP: 8 A 6 G 9 G 12 T 0 other


```

CC breast, testis, ovotestis, bladder, liver, salivary gland, and prostate.
CC and in leukemias and lymphomas. Although the PAP locus contains
CC several identical genes, each at 150, 160, 170, and 180 kb, it is
CC thought that the 150 kb gene may be the most functional gene.
CC The 150 kb gene is the only one that has been found to be
CC transcribed in the adult. The 150 kb gene is the only one that
CC encodes a protein. The protein is a 150 kDa protein and its
CC mutant forms in foetal tissue, placental tissue, amniotic fluid, and
CC serum of a normal people. The method is useful for diagnosis of
CC progressing neoplastic disease. It is becoming a gene in preparation to
CC cancer, for detecting germline and somatic alteration of wild-type APC
CC genes, and for testing therapeutic agents for the ability to suppress
CC tumours. Sequences AAAG388-44001 represent the intron-exon boundary
CC sequences for exons 8-15 of the human APC gene (also referred to as the
CC DP2.5 gene in the specification).
XX
S0 Sequence 29 BP; 11 A; 1 C; 5 G; 12 T; 6 other;
XX
Query Match 49.3%; Score 14.8; DB 2; Length 29;
Best Local Similarity 73.1%; Field No. 4.5e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps
XX
07 4 ATTGGCGGACAGACATTTCTTCTCT 29
XX ||||| ||||| ||||| |||||
XX 4 ATTGGCGGACAGACATTTCTTCTCT 29
XX
RESULT 8
XX ID AAX99849
XX AAX99849;
XX
XX 30-SEP-1999 (first entry)
XX
XX PCR primer CT2 for mouse FGN gene.
XX
XX PCR primer; transgenic animal; mouse; phospholuciferase; FGN; src.
XX
XX Synthetic.
XX Mus sp.
XX
XX JF11102036-A.
XX
XX 21-JUL-1999.
XX
XX 04-JAN-1999; J98F-00030322.
XX
XX 04-JAN-1999; J98F-00030322.
XX
XX 04-JAN-1999; J98F-00030322.
XX
XX (REIKO) KOIKE C.
XX
XX DR 1999-061420/39.
XX
XX New process: useful for preparation of transgene antibody
XX Example 1, page 3, cpg: Japanese.
XX
XX This sequence represents a PCR primer for the mouse phospholuciferase-
XX (pGL3) gene. The invention relates to a process for the preparation of
XX transgenic animals, that comprises: (i) introduction of a foreign gene
XX into foetal cells; (ii) screening of the recombinant cells from the foetal
XX cells for infection of the screened recombinant cells into foetal cells
XX and (iii) transfection of the selected foetal cells into the
XX cells of a foetal animal, foetal animal, and the method is used to prepare
XX transgenic recombinant transgenic animals.
XX
XX Sequence 24 BP; 8 A; 4 C; 10 G; 12 T; 0 other;
XX
Query Match 49.3%; Score 14.8; DB 2; Length 24;
Best Local Similarity 73.1%; Field No. 4.5e+03;
Matches 19; Conservative 0; Mismatches 7; Indels 0; Gaps
XX
5 ATTGGCGGACAGACATTTCTTCTCT 29
XX ||||| ||||| ||||| |||||

```

PT polynucleotide to connexin protein -
 XX
 XX Example 1, Page 17, 4th, English.
 XX
 CC This invention describes a novel formulation (I) for use in therapeutic
 CC and/or cosmetic treatment, comprising at least one antisense
 CC polynucleotide (I), a carrier protein (I) and a carrier with a carrier
 CC vehicle. The polynucleotide (I) is a sense or antisense polynucleotide
 CC having a sequence which is complementary to a sequence of a connexin
 CC protein (II), which is administered to a site on or within a patient
 CC for the specific downregulation of connexin protein expression. (I)
 CC is therefore specifically useful for reducing neuronal cell death
 CC resulting from neuronal insult to a specific site in the brain, spinal
 CC cord or peripheral nerve, for promoting wound healing resulting
 CC from trauma, burns or surgery and for reducing inflammation as a result
 CC of a wound or physical trauma of the brain, spinal cord or optic nerve
 CC and for promoting nerve regeneration in conditions of nerve injury.
 CC Connexin 43 or 31.1 is administered to regulate epithelial basal cell
 CC division and growth or to regulate outer layer keratinization,
 CC respectively, for skin rejuvenation or thickening for cosmetic or
 CC therapeutic purposes in downregulation of connexin expression in a highly
 CC detectable site specific manner. This sequence represents a connexin-43
 CC directed oligonucleotide which is used in the method of the invention.
 XX
 SO Sequence 30 pp, 7 A, 5 C, 9 G, 9 T, 0 other;
 Query Match: 5' 3' Score 17.0, 16.21, Length 60;
 Best Local Similarity: 73.33, Pval: No. 4402;
 Matches: 20, Conserved: 0, Mismatch: 0, Gaps: 0, Nfs: 0;
 QY 1 GTATTGGGACAGAGAAATGTTCTGTC 30
 1 GTATTGGGACAGAGAAATGTTCTGTC 30
 Db 1 GTATTGGGACAGAGAAATGTTCTGTC 30
 RESULT 5
 AAZ87224
 ID AAZ87224 standard; RNA, 27 BP.
 XX
 AC AAZ87224;
 XX
 DT 26 OCT 1998 (first entry)
 XX
 DE Pinctada fucata pearl layer substrate degenerate probe B.
 XX
 KW Pearl oyster, Pearl layer substrate protein; diagenite crystal;
 KW crystalline; synthetic; first, protein; oyster; probe; se
 XX
 OS Synthetic.
 OS Pinctada fucata.
 XX
 PN JP1004009-B1.
 XX
 PD 31 JAN-2000.
 XX
 PF 26 OCT 1998; 98JP 0304179.
 XX
 FR 26 OCT 1998; 98JP 0304179.
 XX
 PA (HAYASHI) HAYASHI N.
 PA (MASUO) MASUO M.
 XX
 DR WPI; 2000 149882/14.
 XX
 PT Pearl layer substrate protein for artificial synthesis of pearl
 PT specific molecular weight of N-terminal and amino acid sequence
 XX
 PS Example 1, Page 5, 14th, Japanese
 XX
 CC The invention relates to the pearl layer substrate protein (sequences
 CC listed above), a synthetic protein of the pearl layer substrate protein
 CC and nucleotide sequences encoding this substrate protein
 CC (AAZ87224-24724). Also claimed is an N-terminal fragment of the

CC substrate protein isolated from the pearl layer (AAZ7714b). This polypep-
 CC fragment was used as the basis for the design of degenerate
 CC oligonucleotide probes (AAZ8722, 24722) for the detection of nucleotide
 CC encoding portions of the substrate protein in a Pinctada fucata pearl
 CC region DNA library. The clones isolated were cloned into a vector
 CC (pRM) amplified using 5' primer and 3' primer from first
 CC (AAZ8722, 24722) and sequenced. The sequence of the first clone
 CC identified was given in AAZ8724 and AAZ8724. This was then cloned into
 CC the pRSE (rapid amplification of cDNA ends) plasmid using PACE primers
 CC AAZ8722-24722. The resulting clones were amplified and sequenced
 CC PCR primers AAZ8722-24722 to give the full length cDNA clones. The
 CC pearl layer substrate protein acts as a model for alternative splicing
 CC formation during the formation of a pearl. Use of the pearl layer
 CC substrate protein may be used in the production of synthetic pearls.
 CC Currently, large-scale pearl production is achieved by cultivation of
 CC pearl oysters. However, pearl formation can take up to two years.
 CC Sequences AAZ8722, 24722 represent a polypeptide protein found in the
 CC sequence of the N-terminal fragment of the pearl layer substrate protein
 CC which were used in an amplification of the present invention.
 XX
 SO Sequence 27 pp, 8 A, 0 C, 6 G, 6 T, 0 other;
 Query Match: 5' 3' Score 15.8, 28.21, Length 27;
 Best Local Similarity: 66.67, Pval: No. 1,6401;
 Matches: 14, Conserved: 4, Mismatch: 3, Gaps: 0, Nfs: 0;
 QY 1 GGGTAAATGAAATGTTTCTT 27
 1 GGGTAAATGAAATGTTTCTT 27
 Db 1 GGGTAAATGAAATGTTTCTT 27
 RESULT 6
 ABL41518
 ID ABL41518 standard; DNA, 24 BP.
 XX
 AC ABL41518;
 XX
 DT 01 JUL 2002 (first entry)
 XX
 DE Primer #2 related to human semaphorin protein 9.
 XX
 KW Human, semaphorin 9, protein; human; human; human; human; human;
 KW nervous system; ss; PCR primer.
 XX
 OS Homo sapiens.
 OS Homo sapiens.
 XX
 PN WO99029496-A1.
 XX
 PD 17 JAN-2002.
 XX
 PF 18 JUN 2001; 2001WO 0209995.
 XX
 FR 18 JUN 2001; 2001WO 0209995.
 XX
 PA (BIOV-) BIOVINDOW GENE DEV INC SHANGHAI.
 PA Mao Y, Xie Y;
 XX
 DR WPI; 2002-106611/14.
 XX
 PT New human semaphorin protein 9 for diagnosing and treating nervous
 PT system deforming and disease associated with functional disturbance of
 PT the nervous system.
 XX
 PS Example 3, Page 12, 37pp; Chinese.
 XX
 CC This invention relates to an isolated polypeptide of human semaphorin
 CC protein 9, thought to be involved in neurite outgrowth in the
 CC action. The proteins and encoding sequences are used in diagnosing and
 CC treatment of nervous system deforming and disease associated with
 CC functional disturbance of the nervous system. The sequence
 CC represents a primer related to semaphorin protein 9.



source 1.21
/organism="unknown"

BASE COUNT 4 a 4 c 5 g 8 t

ORIGIN

Query Match 42.7% Score 12.8, FR 6, Length 21;
Best Local Similarity 97.5% Prod. No. 4.9e+05;
Matches 14, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY 11 CAAGAGATTGTTG 26
DB 20 CAAGAGATTGCTG 5

RESULT 37
LOCUS AR122836
DEFINITION Sequence 19 from Patent US 5650553.
ACCESSION AR122836
VERSION AR122836.1 GI:14107802
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Janjic, N., Gold, L., Schmidt, P. and Varghese, J.
TITLE Vascular endothelial growth factor (VEGF) Nucleic Acid Ligand
JOURNAL
PUBLISHED
FEATURES
Location/Qualifiers
1..23
/organism="unknown"

BASE COUNT 7 a 3 c 10 g 3 t

ORIGIN

Query Match 42.7% Score 12.8, FR 6, Length 23;
Best Local Similarity 97.5% Prod. No. 4.9e+05;
Matches 14, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY 7 GCGGCAAGAGAAATTG 22
DB 1 GCGGTAGAGAAATTG 16

RESULT 38
LOCUS AR122862
DEFINITION Sequence 21 from Patent US 6168703.
ACCESSION AR122862
VERSION AR122862.1 GI:14107828
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 23)
AUTHORS Janjic, N., Gold, L., Schmidt, P. and Varghese, J.
TITLE Vascular endothelial growth factor (VEGF) Nucleic Acid Ligand
JOURNAL
PUBLISHED
FEATURES
Location/Qualifiers
1..23
/organism="unknown"

BASE COUNT 7 a 3 c 10 g 3 t

ORIGIN

Query Match 42.7% Score 12.8, FR 6, Length 23;
Best Local Similarity 97.5% Prod. No. 4.9e+05;
Matches 14, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY 7 GCGGCAAGAGAAATTG 22
DB 1 GCGGTAGAGAAATTG 16

RESULT 39
LOCUS 157019
DEFINITION Sequence 19 from Patent US 5650553.
ACCESSION 157019
VERSION 157019.1 GI:14107422
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 24)
AUTHORS Ecker, J., Rothenberg, M., Lehman, A. and Roman, G.
TITLE Plant Genes for sensitivity to ethylene and pathogen
JOURNAL
PUBLISHED
FEATURES
Location/Qualifiers
1..24
/organism="unknown"

BASE COUNT 7 a 5 c 4 g 8 t

ORIGIN

Query Match 42.7% Score 12.8, FR 6, Length 24;
Best Local Similarity 97.5% Prod. No. 4.9e+05;
Matches 17, Conservative 0, Mismatches 7, Indels 0, Gaps 0

CY 6 TGGGCAAGAGAAATTGTTGTTG 29
DB 1 TGGGCAAGAGAAATTGTTGTTG 24

RESULT 40
LOCUS AX214402
DEFINITION Sequence 10 from Patent WO0159450.
ACCESSION AX214402
VERSION AX214402.1 GI:15521476
KEYWORDS
SOURCE
ORGANISM
REFERENCE 1 (bases 1 to 29)
AUTHORS
TITLE Cells for drug discovery
JOURNAL
PUBLISHED
FEATURES
Location/Qualifiers
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/organism="synthetic construct"
/db_xref="taxon:32630"
/note="primer SPB7"

BASE COUNT 12 a 6 c 9 g 2 t

ORIGIN

Query Match 42.7% Score 12.8, FR 6, Length 24;
Best Local Similarity 97.5% Prod. No. 4.9e+05;
Matches 14, Conservative 0, Mismatches 2, Indels 0, Gaps 0

CY 4 ATTGGGCAAGAGAA 19
DB 7 ATTGGGCAAGAGAA 22

Search completed: July 23, 2003, 14:34:39
Job time : 329.497 secs

COMPANY: The Scripts Research Institute (TSR)
 COUNTRY: U.S.A.
 DATE: 1992-02-13
 FEATURES: Location/Qualifiers
 SOURCE: 1.35

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/db_xref="tacon.32620"
/feature="PCR setup" /first for sequencing EAV-1 light chain
for whole analysis of PCR products..."
11 a 11 c 7 g 6 t

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[illegible]

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AR094621/c	
DEFINITION	AR094621 23 bp. DNA
ACCESSION	AR094621
VERSION	AR094621.1 01-JAN-1999
KEYWORDS	
SOURCE	Unknown
ORGANISM	Unknown
	linear PAT vs-SRP-2000

REFERENCE	AUTHORS	TITLE	JOURNAL	YEAR	ISSUE	PAGES	ABSTRACTS	Source
1 (bases 1 to 2)	Benjamin D. J. and Yanagisawa M.	Effects of the morphological structure of the	Journal of the	1990	1	1-14		location/Qualifiers
2				1990	1	1-14		1. 23
3				1990	1	1-14		/organism="unknown"
4				1990	1	1-14		

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Best local similarity for coverage of Matched	5	100%	0	0.00
27	10	GCAGAGAAATGTTCTGTC	30	
28	11		31	
29	22	GCACAGAAAGCGTTCTCTGCC	2	

RESULT	29
ARI75701/c	
STATUS	ARI75701
DEFINITION	Sequence 16 from patent DE 680004
ACCESSION	ARI75701
VERSION	ARI75701.1 GI:175701000
KEYWORDS	
SOURCE	Unknown
ORGANISM	

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organism="unknown"
REFERENCE
  Unclassified:
  1 bases (1 to 23)
AUTHORS
  Bergsma J D, Brinkhof A, Grollman A P, van der
  Pol-Anaar J, van der Pol-Anaar J, van der Pol-Anaar
  J, van der Pol-Anaar J, van der Pol-Anaar J,
  HPGAN72
FEATURES
  Location: 1 to 23
  Location/Qualifiers
    1..23
    /organism="unknown"
SOURCE

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CASTLE POINT	4	3	2	1
Very Much	43.3%	Score 13	DR 6	Length 23
Mostly	33.3%	Score 12	DR 5	Length 22
Medium	16.7%	Score 11	DR 4	Length 21
Little	4.0%	Score 10	DR 3	Length 20
Not at all	3.7%	Score 9	DR 2	Length 19

27 10 GCAAGAGAAATGTTCTGTC 30
 22 GCGAGAGAGCTGTTCCTGCC 2
 Db

RESULT 30	ED6917
ED6917.C	Ed6917
LOCUS	Ed6917
DEFINITION	Clinonucleotide primer, anti

REFERENCE	ORGANISM	SOURCE	VERSION	ACCESSION
1 (bases 1 to 23)	Hepatitis C virus			F06917
	Hepatitis C virus			F06918
	Hepatitis C virus			F06919
	Hepatitis C virus			F06920
	Hepatitis C virus			F06921
	Hepatitis C virus			F06922
	Hepatitis C virus			F06923
	Hepatitis C virus			F06924
	Hepatitis C virus			F06925
	Hepatitis C virus			F06926
	Hepatitis C virus			F06927
	Hepatitis C virus			F06928
	Hepatitis C virus			F06929
	Hepatitis C virus			F06930
	Hepatitis C virus			F06931
	Hepatitis C virus			F06932
	Hepatitis C virus			F06933
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	Hepatitis C virus			F06998
	Hepatitis C virus			F06999
	Hepatitis C virus			F07000

COMMENT	AUTHOR'S TITLE
OS Hepatitis C virus	OROSHIMA AND KAWANISHI, T. METHOD FOR DETECTING HEPATITIS C VIRUS IN HUMAN SERUM BY ELISA
EN JP 1994000606/6	Patent: JP 1994000606 A 6 IMMO JAPAN:XX
EP 15-MAR-1994	
FF 26-NOV-1994	
FI 26-NOV-1994	
FR 26-NOV-1994	
GR 26-NOV-1994	
IT 26-NOV-1994	
JP 26-NOV-1994	
SE 26-NOV-1994	
SI 26-NOV-1994	
SK 26-NOV-1994	
TR 26-NOV-1994	
UK 26-NOV-1994	
US 26-NOV-1994	
WO 26-NOV-1994	
ZA 26-NOV-1994	
Other countries: Single	

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FEATURES
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    topology: linear;
    cc: hyperbolic; NO;
    cc: antisense: Yes;
    location: Gallio;
    1: 23;
    /organism: "Hepati
    /db_xref: "taxon:1
  7 a      6 c      7

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Query Match: 43.3% Score
Best Local Similarity: 70.0% E-Value
Method: BLAST, Insulating: 0, Masking: 0

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RESULT 31
AX249699
LOCUS AX249699
LENGTH 1000
REFERENCE AX249699
VERSION AX249699
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens

[illegible]

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BASE COUNT      11 a /cd_xcif=txconf
ORIGIN           3 c
Serial Number    4 i s t score
Serial Count     6 e o d f tcount
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PC	(C121217)CC(C121218)CC(C121219)
CC	Strandedness: Single
CC	Topology: Linear;
FH	Key
FT	source
PT	Location/Qual value

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	/origin="not_defined"
	/db_xref="taxon:2844"
BASE COUNT	5 a 9 c 7 g 6 t
ORIGIN	

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Best Local Similarity:	40.66	Prod. No. 1.000	
Matches: 16,	Conservative: 0,	Mismatches: 4,	Indels: 0,
			Gaps: 0

cy 9 GGCAGAGAAATGTTCTG 28
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 id 8 GGTGAGAGAACTGCTTCTG 27

[illegible]

REFERENCE	UNCLASSIFIED	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
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THOMAS	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
JOHNSTON	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100	
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[illegible][illegible]

FEATURE	LOCATION/Qualifiers
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	/Organism="Synthetic construct"
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BASE COUNT	6..7..5..6..
ORIGIN	6..6..5..6..

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QY 7 GCGGCAAGAGAAATGGTTCTGT 28
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RESULT 23	BD013251			
LOCUS				
DEFINITION	BD013251	27 bp	DNA	100000
ACCESSION	BD013251			
VERSION	BD013251.1	GI:22039440		
KEYWORDS	W0 01.03.96 A/11.			
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	Maeda,M. and Tasachi,N.			
TITLE	Novel hemopoietin receptor protein, NR12			
JOURNAL	FEBS LETT 364:11-15 (1995)			
COMMENT	GENE: RESEARCH INSTITUTE FOR MOLECULAR MEDICINE CO., NAGANO			
	MEDA, NORIKO YASUCHI			
OS	Artificial Sequence			

[illegible]

Query Match	Score	DB ID	Length
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Query 2	44.77	DB 67	100
Query 3	44.77	DB 67	100
Query 4	44.77	DB 67	100
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Query 7	44.77	DB 67	100
Query 8	44.77	DB 67	100
Query 9	44.77	DB 67	100
Query 10	44.77	DB 67	100
Query 11	44.77	DB 67	100
Query 12	44.77	DB 67	100
Query 13	44.77	DB 67	100
Query 14	44.77	DB 67	100
Query 15	44.77	DB 67	100
Query 16	44.77	DB 67	100
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Query 24	44.77	DB 67	100
Query 25	44.77	DB 67	100
Query 26	44.77	DB 67	100
Query 27	44.77	DB 67	100
Query 28	44.77	DB 67	100
Query 29	44.77	DB 67	100
Query 30	44.77	DB 67	100
Query 31	44.77	DB 67	100
Query 32	44.77	DB 67	100
Query 33	44.77	DB 67	100
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87
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 Db

29
 24

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RESULT 24
H0102170
ID BD010219 standard, DNA, SVT; 27 BP.
XX
AC H0010219;
XX
SV BD010219.1
XX
08-FEB-2002 (Rel. 70, Created)
BT

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ORIGIN

Query Match 47.3% Score 14.2; DB 6; Length 30;
 Best Local Similarity 70.4% Prod. No. 17605;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CY 3 AATTGGCGAAGAGATTGTTCTGT 29
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RESULT 12
 E31861
 LOCUS E31861
 DEFINITION Novel cancer metastasis marker
 ACCESSION E31861
 VERSION E31861.1 GI:11971422
 KEYWORDS CD144;A1414
 SOURCE unidentifed
 ORGANISM unidentifed

REFERENCE 1 (bases 1 to 22)
 AUTHORS Masamitsu T, Mami S, Fujitsugu H, and Ikumochi Y
 TITLE Novel cancer metastasis marker
 JOURNAL Patent: JP 199913591 A 15 Nov 1999,
 TAYLOR FRANKLIN LTD
 COMMENT CC Unidentifed
 PN JP 199913591 A/15
 PR 16-NOV-1999
 RF CI MAY 1999 JP 1999-1163

FEATURES
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 /db_xref="taxon:32644"

BASE COUNT 6 a 6 c 5 g 5 t
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 Best Local Similarity 70.4% Prod. No. 17605;
 Matches 15; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

CY 6 TGGCGAAGAGATTGTTCTGT 29
 |||||
 22 TGGCGAAGAGATTGTTCTGT 1

RESULT 13
 AR122834
 LOCUS AR122834
 DEFINITION Sequence 56 bp from patent US 6168778.
 ACCESSION AR122834
 VERSION AR122834.1 GI:114107800
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown

REFERENCE 1 (bases 1 to 29)
 AUTHORS Janjic N, Gold L, Schmidt P, and Vargese C
 TITLE Vascular endothelial growth factor (VEGF) Nucleic Acid Ligand
 Complexes
 JOURNAL Patent: US 6168778 A 06 Oct 2001,
 FEATURES
 1..28 Location/Qualifiers
 source /organism="unknown"

BASE COUNT 9 a 3 c 12 g 4 t
 ORIGIN

Query Match 46.0% Score 13.8; DB 6; Length 30;
 Best Local Similarity 70.4% Prod. No. 17605;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 6 TGGCGAAGAGATTGTTCTGT 22
 |||||
 6 TGGCGAAGAGATTGTTCTGT 22

RESULT 14
 AR122835
 LOCUS AR122835
 DEFINITION Sequence 57 bp from patent US 6168778.
 ACCESSION AR122835
 VERSION AR122835.1 GI:114107801
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown

REFERENCE 1 (bases 1 to 28)
 AUTHORS Janjic N, Gold L, Schmidt P, and Vargese C
 TITLE Vascular endothelial growth factor (VEGF) Nucleic Acid Ligand
 Complexes
 JOURNAL Patent: US 6168778 A 06 Oct 2001,
 FEATURES
 1..28 Location/Qualifiers
 source /organism="unknown"

BASE COUNT 9 a 4 c 11 g 4 t
 ORIGIN
 Query Match 46.0% Score 13.8; DB 6; Length 30;
 Best Local Similarity 89.2% Prod. No. 17605;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 6 TGGCGAAGAGATTGTTCTGT 22
 |||||
 5 TGGCGAAGAGATTGTTCTGT 21

RESULT 15
 AR122852
 LOCUS AR122852
 DEFINITION Sequence 29 bp from patent US 6168778.
 ACCESSION AR122852
 VERSION AR122852.1 GI:114107818
 KEYWORDS
 SOURCE Unknown
 ORGANISM Unknown

REFERENCE 1 (bases 1 to 29)
 AUTHORS Janjic N, Gold L, Schmidt P, and Vargese C
 TITLE Vascular endothelial growth factor (VEGF) Nucleic Acid Ligand
 Complexes
 JOURNAL Patent: US 6168778 A 06 Oct 2001,
 FEATURES
 1..29 Location/Qualifiers
 source /organism="unknown"

BASE COUNT 9 a 4 c 12 g 4 t
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 Best Local Similarity 89.2% Prod. No. 17605;
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

CY 6 TGGCGAAGAGATTGTTCTGT 22
 |||||
 6 TGGCGAAGAGATTGTTCTGT 22

RESULT 16
 DB 6 TGGCGAAGAGATTGTTCTGT 22

FEATURES

source

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 89.3% Score 26.8, E: 6, Length 30;
 Best Local Similarity: 92.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 30 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

RESULT 4

AX012931

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 89.3% Score 26.8, E: 6, Length 30;
 Best Local Similarity: 92.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 30 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

FEATURES

source

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 89.3% Score 26.8, E: 6, Length 30;
 Best Local Similarity: 92.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 30 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

RESULT 5

AX012931

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 89.3% Score 26.8, E: 6, Length 30;
 Best Local Similarity: 92.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 30 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

FEATURES

source

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 89.3% Score 26.8, E: 6, Length 30;
 Best Local Similarity: 92.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Query Match: 57.3% Score 17.2, E: 6, Length 30;
 Best Local Similarity: 73.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 1 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

RESULT 6

AX128301

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 57.3% Score 17.2, E: 6, Length 30;
 Best Local Similarity: 73.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 1 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

FEATURES

source

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 57.3% Score 17.2, E: 6, Length 30;
 Best Local Similarity: 73.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 1 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

RESULT 7

E16238

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 57.3% Score 17.2, E: 6, Length 30;
 Best Local Similarity: 73.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 1 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

FEATURES

source

Location/Qualifiers

BASE COUNT

10 a 10 c 4 g 6 t

Query Match: 57.3% Score 17.2, E: 6, Length 30;
 Best Local Similarity: 73.3% Prod. No. 0.06;
 Matches: 28, Conservative: 17, Mismatches: 4, Indels: 0, Gaps: 0;

Db: 1 GATATGCGGACAGAGAAATGTTCTGTC 30
 1 GATATGCGGACAGAGAAATGTTCTGTC 30

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SUMMARIES

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

```

CM nucleotide nucleotide search, using sw-nw-hi
Run on:      July 21, 2003, 10:41:07, Search time 211.198 seconds
              (without alignments)
              2502.265 Million cell alignments
Title:       US-09-890-363-1
Perfect score: 30
Sequences:   1: gtaattggcggaagagagattggttcggttc
Scoring table: IDENTITY NUC
              Gap: 10.0, Open: 1.0
Searched:    2094640 Popen: 14551400929 residues
Total number of hits satisfying chosen parameters: 66630
Minimum DB seq length: 0
Maximum DB seq length: 35
Post-processing: Minimum Match 03
                  Maximum Match 1000
                  Listing first 1000 summaries
Database:      GenBank
1: gb-ba:*
2: gb-ba:*
3: gb-ba:*
4: gb-ba:*
5: gb-ba:*
6: gb-ba:*
7: gb-ba:*
8: gb-ba:*
9: gb-ba:*
10: gb-ba:*
11: gb-ba:*
12: gb-ba:*
13: gb-ba:*
14: gb-ba:*
15: gb-ba:*
16: gb-ba:*
17: gb-ba:*
18: gb-ba:*
19: gb-ba:*
20: gb-ba:*
21: gb-ba:*
22: gb-ba:*
23: gb-ba:*
24: gb-ba:*
25: gb-ba:*
26: gb-ba:*
27: gb-ba:*
28: gb-ba:*
29: gb-ba:*
30: gb-ba:*
31: gb-ba:*
32: gb-ba:*
33: gb-ba:*
34: gb-ba:*
35: gb-ba:*
36: gb-ba:*
37: gb-ba:*
38: gb-ba:*
39: gb-ba:*
40: gb-ba:*
41: gb-ba:*

```

Result No.	Score	% Match	Query Length	DB ID	Description
1	30	100.0	30	AX032823	AX032823 Sequence
2	28.8	96.0	30	AX032824	AX032824 Sequence
3	26.8	89.3	30	AX032825	AX032825 Sequence
4	26.8	89.3	30	AX032826	AX032826 Sequence
5	17.2	57.3	30	AX032827	AX032827 Sequence
6	14.8	49.3	30	AX032828	AX032828 Sequence
7	14.8	49.3	35	E16238	E16238 PCR Primer
8	14.8	49.3	35	E16239	E16239 PCR Primer
9	14.2	47.3	27	AX454981	AX454981 Sequence
10	14.2	47.3	30	AX107179	AX107179 Sequence
11	14.2	47.3	22	E31861	E31861 Novel Gene
12	14.2	47.3	22	E31862	E31862 Novel Gene
13	14.2	47.3	22	E31863	E31863 Novel Gene
14	14.2	47.3	22	E31864	E31864 Novel Gene
15	14.2	47.3	22	E31865	E31865 Novel Gene
16	14.2	47.3	22	E31866	E31866 Novel Gene
17	14.2	47.3	22	E31867	E31867 Novel Gene
18	14.2	47.3	22	E31868	E31868 Novel Gene
19	14.2	47.3	22	E31869	E31869 Novel Gene
20	14.2	47.3	22	E31870	E31870 Novel Gene
21	14.2	47.3	22	E31871	E31871 Novel Gene
22	14.2	47.3	22	E31872	E31872 Novel Gene
23	14.2	47.3	22	E31873	E31873 Novel Gene
24	14.2	47.3	22	E31874	E31874 Novel Gene
25	14.2	47.3	22	E31875	E31875 Novel Gene
26	14.2	47.3	22	E31876	E31876 Novel Gene
27	14.2	47.3	22	E31877	E31877 Novel Gene
28	14.2	47.3	22	E31878	E31878 Novel Gene
29	14.2	47.3	22	E31879	E31879 Novel Gene
30	14.2	47.3	22	E31880	E31880 Novel Gene
31	14.2	47.3	22	E31881	E31881 Novel Gene
32	14.2	47.3	22	E31882	E31882 Novel Gene
33	14.2	47.3	22	E31883	E31883 Novel Gene
34	14.2	47.3	22	E31884	E31884 Novel Gene
35	14.2	47.3	22	E31885	E31885 Novel Gene
36	14.2	47.3	22	E31886	E31886 Novel Gene
37	14.2	47.3	22	E31887	E31887 Novel Gene
38	14.2	47.3	22	E31888	E31888 Novel Gene
39	14.2	47.3	22	E31889	E31889 Novel Gene
40	14.2	47.3	22	E31890	E31890 Novel Gene
41	14.2	47.3	22	E31891	E31891 Novel Gene
42	14.2	47.3	22	E31892	E31892 Novel Gene
43	14.2	47.3	22	E31893	E31893 Novel Gene
44	14.2	47.3	22	E31894	E31894 Novel Gene
45	14.2	47.3	22	E31895	E31895 Novel Gene
46	14.2	47.3	22	E31896	E31896 Novel Gene
47	14.2	47.3	22	E31897	E31897 Novel Gene
48	14.2	47.3	22	E31898	E31898 Novel Gene
49	14.2	47.3	22	E31899	E31899 Novel Gene
50	14.2	47.3	22	E31900	E31900 Novel Gene
51	14.2	47.3	22	E31901	E31901 Novel Gene
52	14.2	47.3	22	E31902	E31902 Novel Gene
53	14.2	47.3	22	E31903	E31903 Novel Gene
54	14.2	47.3	22	E31904	E31904 Novel Gene
55	14.2	47.3	22	E31905	E31905 Novel Gene
56	14.2	47.3	22	E31906	E31906 Novel Gene
57	14.2	47.3	22	E31907	E31907 Novel Gene
58	14.2	47.3	22	E31908	E31908 Novel Gene
59	14.2	47.3	22	E31909	E31909 Novel Gene
60	14.2	47.3	22	E31910	E31910 Novel Gene
61	14.2	47.3	22	E31911	E31911 Novel Gene
62	14.2	47.3	22	E31912	E31912 Novel Gene
63	14.2	47.3	22	E31913	E31913 Novel Gene
64	14.2	47.3	22	E31914	E31914 Novel Gene
65	14.2	47.3	22	E31915	E31915 Novel Gene
66	14.2	47.3	22	E31916	E31916 Novel Gene
67	14.2	47.3	22	E31917	E31917 Novel Gene

Pred. No. 15: the number of results predicted by the software.